

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
13 September 2001 (13.09.2001)

PCT

(10) International Publication Number  
**WO 01/66573 A2**

(51) International Patent Classification<sup>7</sup>: C07K 14/34

(21) International Application Number: PCT/IB00/02035

(22) International Filing Date:  
22 December 2000 (22.12.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  
60/187,970 9 March 2000 (09.03.2000) US  
09/606,740 23 June 2000 (23.06.2000) US

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,  
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,  
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,  
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,  
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,  
TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,  
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian  
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European  
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,  
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,  
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

**Published:**

--- without international search report and to be republished  
upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guid-  
ance Notes on Codes and Abbreviations" appearing at the begin-  
ning of each regular issue of the PCT Gazette.

(54) Title: *CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING METABOLIC PATHWAY PROTEINS

(57) Abstract: Isolated nucleic acid molecules, designated MP nucleic acid molecules, which encode novel MP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated MP proteins, mutated MP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MP genes in this organism.

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## ***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING METABOLIC PATHWAY PROTEINS**

### **Related Applications**

5       The present application is an continuation in part of U.S. Patent Application  
09/606,740, filed June 23, 2000. This application is also a continuation in part of U.S.  
Patent Application 09/603,124, filed June 23, 2000. The present application claims  
priority to prior filed U.S. Provisional Patent Application Serial No. 60/141031, filed  
June 25 , 1999, U.S. Provisional Patent Application Serial No. 60/142101, filed July 2,  
10   1999, U.S. Provisional Patent Application Serial No. 60/148613, filed August 12, 1999,  
U.S. Provisional Patent Application Serial No. 60/187970, filed March 9, 2000, and also  
to German Patent Application No. 19931420.9, filed July 8, 1999. The entire contents  
of all of the aforementioned applications are hereby expressly incorporated herein by  
this reference.

15

### **Background of the Invention**

Certain products and by-products of naturally-occurring metabolic processes in  
cells have utility in a wide array of industries, including the food, feed, cosmetics, and  
pharmaceutical industries. These molecules, collectively termed 'fine chemicals',  
20   include organic acids, both proteinogenic and non-proteinogenic amino acids,  
nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic  
compounds, vitamins and cofactors, and enzymes. Their production is most  
conveniently performed through large-scale culture of bacteria developed to produce  
and secrete large quantities of a particular desired molecule. One particularly useful  
25   organism for this purpose is *Corynebacterium glutamicum*, a gram positive,  
nonpathogenic bacterium. Through strain selection, a number of mutant strains have  
been developed which produce an array of desirable compounds. However, selection of  
strains improved for the production of a particular molecule is a time-consuming and  
difficult process.

30

### **Summary of the Invention**

The invention provides novel bacterial nucleic acid molecules which have a  
variety of uses. These uses include the identification of microorganisms which can be

used to produce fine chemicals (*e.g.*, amino acids, such as, for example, lysine and methionine), the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation.

- 5 These novel nucleic acid molecules encode proteins, referred to herein as metabolic pathway (MP) proteins.

*C. glutamicum* is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of  
10 terpenoids. The MP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the MP nucleic acids of the invention, or modification of the sequence of the MP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a  
15 microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species). In a preferred embodiment, the MP genes of the invention are combined with one or more genes involved in the same or different metabolic pathway to modulate the production of one or more fine chemicals from a microorganism.

- 20 The MP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or  
25 mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of  
30 significant clinical relevance.

The MP nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms.

Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The MP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing an enzymatic step involved in the metabolism of certain fine chemicals, including amino acids, *e.g.*, lysine and methionine, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals.

This improved production or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation. Specifically, alterations in *C. glutamicum* metabolic pathways for amino acids, *e.g.*, lysine and methionine, vitamins, cofactors, nucleotides, and trehalose may have a direct impact on the overall production of one or more of these desired compounds from this organism. For example, optimizing the activity of a lysine or a methionine biosynthetic pathway protein or decreasing the activity of a lysine or methionine degradative pathway protein may result in an increase in the yield or efficiency of production of lysine or methionine from such an engineered organism. Alterations in the proteins involved in these metabolic pathways may also have an indirect impact on the production or efficiency of production of a desired fine chemical. For example, a reaction which is in competition for an intermediate necessary for the production of a desired molecule may be eliminated, or a pathway necessary for the production of a particular intermediate for a desired compound may be optimized. Further, modulations in the biosynthesis or degradation of, for example, an amino acid, *e.g.*, lysine or methionine, a vitamin, or a nucleotide may increase the overall ability of the microorganism to rapidly grow and divide, thus increasing the number and/or production capacities of the microorganism in culture and thereby increasing the possible yield of the desired fine chemical.



The nucleic acid and protein molecules of the invention, alone or in combination with one or more nucleic acid and protein molecules of the same or different metabolic pathway, may be utilized to directly improve the production or efficiency of production of one or more desired fine chemicals from *Corynebacterium glutamicum* (e.g., methionine or lysine). Using recombinant genetic techniques well known in the art, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, e.g., lysine and methionine, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of the desired fine chemical may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of other fine chemicals besides the amino acids, e.g., lysine and methionine, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose through indirect mechanisms. Metabolism of any one compound is necessarily intertwined with other biosynthetic and degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway. Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins, may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

This invention provides novel nucleic acid molecules which encode proteins, referred to herein as metabolic pathway ("MP") proteins, which are capable of, for

example, performing an enzymatic step involved in the metabolism of molecules important for the normal functioning of cells, such as amino acids, *e.g.*, lysine and methionine, vitamins, cofactors, nucleotides and nucleosides, or trehalose. Nucleic acid molecules encoding an MP protein are referred to herein as MP nucleic acid molecules.

- 5 In a preferred embodiment, an MP protein, alone or in combination with one or more proteins of the same or different metabolic pathway, performs an enzymatic step related to the metabolism of one or more of the following: amino acids, *e.g.*, lysine and methionine, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Examples of such proteins include those encoded by the genes set forth in Table 1.

- 10 Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MP-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments,
- 15 the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or
- 20 is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% or
- 25 more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6). The preferred MP
- 30 proteins of the present invention also preferably possess at least one of the MP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence

which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence having an even-numbered SEQ ID NO in the Sequence Listing, such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an MP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform an enzymatic reaction in a amino acid, *e.g.*, lysine or methionine, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected from those having an even-numbered SEQ ID NO in the Sequence Listing, such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5)).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an MP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing, such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6) and is able to catalyze a reaction in a metabolic pathway for an amino acid, *e.g.*, lysine or methionine, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose, or one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-

numbered SEQ ID NO in the Sequence Listing, such as SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5). Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, alone or in combination with one or more nucleic acid molecules involved in the same or different pathway, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MP protein by culturing the host cell in a suitable medium. The MP protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which one or more MP genes, alone or in combination with one or more genes involved in the same or different metabolic pathway, have been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding one or more wild-type or mutated MP sequences as transgenes alone or in combination with one or more nucleic acid molecules involved in the same or different metabolic pathway. In another embodiment, one or more endogenous MP genes within the genome of the microorganism have been altered, *e.g.*, functionally disrupted, by homologous recombination with one or more altered MP genes. In another embodiment, one or more endogenous or introduced MP genes, alone or in combination with one or more genes of the same or different metabolic pathway in a microorganism have been altered by one or more point mutations, deletions, or inversions, but still encode functional MP proteins. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of one or more MP genes in a microorganism, alone or in combination with one or more MP genes or in combination with one or more genes of the same or different metabolic pathway, has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of one or more MP genes is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine and

methionine being particularly preferred. In a particularly preferred embodiment, the MP gene is the *metZ* gene (SEQ ID NO:1), *metC* gene (SEQ ID NO:3), or the RXA00657 gene (SEQ ID NO:5), alone or in combination with one or more MP genes of the invention or in combination with one or more genes involved in methionine and/or lysine metabolism.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth in Table 1 and in the Sequence Listing as SEQ ID NOs 1 through 122) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated MP protein or portion, e.g., biologically active portion, thereof. In a preferred embodiment, the isolated MP protein or portion thereof, alone or in combination with one or more MP proteins of the invention or in combination with one or more proteins of the same or different metabolic pathway, can catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, e.g., lysine or methionine, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose. In another preferred embodiment, the isolated MP protein or portion thereof, is sufficiently homologous to an amino acid sequence of the invention (e.g., a sequence of an even-numbered SEQ ID NO: in the Sequence Listing, such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6) such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.

The invention also provides an isolated preparation of an MP protein. In preferred embodiments, the MP protein comprises an amino acid sequence of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention (e.g., a sequence of an even-numbered SEQ ID NO of the Sequence Listing such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing such as SEQ ID

NO:1, SEQ ID NO:3, or SEQ ID NO:5). In yet another embodiment, the protein is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% or more homologous to an entire amino acid sequence of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6). In other embodiments, the isolated MP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6) and is able to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway either alone or in combination one or more MP proteins of the invention or any protein of the same or different metabolic pathway, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated MP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, or is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% or more homologous to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of MP proteins also have one or more of the MP bioactivities described herein.

The MP polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MP protein alone. In other preferred embodiments, this fusion protein, when introduced into a *C. glutamicum* pathway for the metabolism of an amino acid, vitamin, cofactor, nutraceutical, results in increased yields and/or efficiency of production of a desired fine chemical from *C. glutamicum*. In particularly preferred embodiments, integration of this fusion protein

into an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway of a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing one or more vectors directing the expression of one or more MP nucleic acid molecules of the either alone or in combination one or more MP nucleic acid molecules of the invention or any nucleic acid molecule of the same or different metabolic pathway, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an MP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3. In another preferred embodiment, the MP genes is the *metZ* gene (SEQ ID NO:1), *metC* gene (SEQ ID NO:3), or the gene designated as RXA00657 (SEQ ID NO:5) (see Table 1), alone or in combination with one or more MP nucleic acid molecules of the invention or with one or more genes involved in methionine and/or lysine metabolism. In yet another preferred embodiment, the fine chemical is an amino acid, e.g., L-lysine and L-methionine.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates MP protein activity or MP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates MP protein activity can be an agent which stimulates MP protein activity or MP nucleic acid expression. Examples of agents which stimulate MP protein activity or MP nucleic acid expression

include small molecules, active MP proteins, and nucleic acids encoding MP proteins that have been introduced into the cell. Examples of agents which inhibit MP activity or expression include small molecules and antisense MP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a  
5 desired compound from a cell, involving the introduction of a wild-type or mutant MP gene into a cell, either alone or in combination one or more MP nucleic acid molecules of the invention or any nucleic acid molecule of the same or different metabolic pathway, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take  
10 place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino  
15 acid are L-lysine and L-methionine. In another preferred embodiment, said gene is the *metZ* gene (SEQ ID NO:1), *metC* gene (SEQ ID NO:3), or the RXA00657 gene (SEQ ID NO:5), alone or in combination with one or more MP nucleic acid molecules of the invention or with one or more genes involved in methionine and/or lysine metabolism.

## 20 Detailed Description of the Invention

The present invention provides MP nucleic acid and protein molecules which are involved in the metabolism of certain fine chemicals in *Corynebacterium glutamicum*, including amino acids, *e.g.*, lysine and methionine, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. The molecules of the invention may be utilized  
25 in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where modulation of the activity of a lysine or methionine biosynthesis protein has a direct impact on the production or efficiency of production of lysine or methionine from that organism), or may have an indirect impact which nonetheless results in an increase of yield or efficiency of production of the  
30 desired compound (*e.g.*, where modulation of the activity of a nucleotide biosynthesis protein has an impact on the production of an organic acid or a fatty acid from the bacterium, perhaps due to improved growth or an increased supply of necessary co-factors, energy compounds, or precursor molecules). The MP molecules may be utilized



alone or in combination with other MP molecules of the invention, or in combination with other molecules involved in the same or a different metabolic pathway (*e.g.*, lysine or methionine metabolism). In a preferred embodiment, the MP molecules are the *metZ* (SEQ ID NO:1), *metC* (SEQ ID NO:3), or RXA00657 (SEQ ID NO:5) nucleic acid molecules and the proteins encoded by these nucleic acid molecules (SEQ ID NO:2, SEQ ID NO:4 and SEQ ID NO:6, respectively). Aspects of the invention are further explicated below.

### I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in *Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) *Chemicals by Fermentation*, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

#### A. Amino Acid Metabolism and Uses

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-

recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH:

- 5 Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins.

- Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3<sup>rd</sup> edition, pages 578-590 (1988)). The 'essential' amino acids
- 10 (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals
- 15 do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

- Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical
- 20 industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine,
- 25 valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be
- 30 useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of  $\alpha$ -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain  $\beta$ -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine.

The biosynthetic pathways leading to methionine have been studied in diverse organisms. The first step, acylation of homoserine, is common to all of the organisms, even though the source of the transferred acyl groups is different. *Escherichia coli* and the related species use succinyl-CoA (Michaeli, S. and Ron, E. Z. (1981) *Mol. Gen. Genet.* 182, 349-354), while *Saccharomyces cerevisiae* (Langin, T., et al. (1986) *Gene* 49, 283-293), *Brevibacterium flavum* (Miyajima, R. and Shiio, I. (1973) *J. Biochem.* 73, 1061-1068; Ozaki, H. and Shiio, I. (1982) *J. Biochem.* 91, 1163-1171), *C. glutamicum* (Park, S.-D., et al. (1998) *Mol. Cells* 8, 286-294), and *Leptospira meyeri* (Belfaiza, J. et al. (1998) 180, 250-255; Bourhy, P., et al. (1997) *J. Bacteriol.* 179, 4396-4398) use acetyl-CoA as the acyl donor. Formation of homocysteine from acylhomoserine can occur in two different ways. *E. coli* uses the transsulfuration pathway which is catalyzed by cystathionine  $\gamma$ -synthase (the product of *metB*) and cystathionine  $\beta$ -lyase

(the product of *metC*). *S. cerevisiae* (Cherest, H. and Surdin-Kerjan, Y. (1992) *Genetics* 130, 51-58), *B. flavum* (Ozaki, H. and Shio, I. (1982) *J. Biochem.* 91, 1163-1171), *Pseudomonas aeruginosa* (Foglino, M., et al. (1995) *Microbiology* 141, 431-439), and *L. meyeri* (Belfaiza, J., et al. (1998) *J. Bacteriol.* 180, 250-255) utilize the direct  
5    sulfhydrylation pathway which is catalyzed by acylhomoserine sulfhydrylase. Unlike closely related *B. flavum* which uses only the direct sulfhydrylation pathway, enzyme activities of the transsulfuration pathway have been detected in the extracts of the *C. glutamicum* cells and the pathway has been proposed to be the route for methionine biosynthesis in the organism (Hwang, B-J., et al. (1999) *Mol. Cells* 9, 300-308; Kase, H.  
10    and Nakayama, K. (1974) *Agr. Biol. Chem.* 38, 2021-2030; Park, S.-D., et al. 1998) *Mol. Cells* 8, 286-294).

Although some genes involved in methionine biosynthesis in *C. glutamicum* have been isolated, information on the biosynthesis of methionine in *C. glutamicum* is still very limited. No genes other than *metA* and *metB* have been isolated from the  
15    organism. To understand the biosynthetic pathways leading to methionine in *C. glutamicum*, we have isolated and characterized the *metC* gene (SEQ ID NO:3) and the *metZ* (also called *metY*) gene (SEQ ID NO:1) of *C. glutamicum* (see Table 1).

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of  
20    the cell (for review see Stryer, L. Biochemistry 3<sup>rd</sup> ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition,  
25    in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3<sup>rd</sup> ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

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#### *B. Vitamin, Cofactor, and Nutraceuical Metabolism and Uses*

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although

they are readily synthesized by other organisms, such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCs Press: Champaign, IL X, 374 S).

Thiamin (vitamin B<sub>1</sub>) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B<sub>2</sub>) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B<sub>6</sub>' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- $\beta$ -alanine) can be produced

either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of  $\beta$ -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to  $\beta$ -alanine and for the condensation to panthotenic acid are known. The metabolically  
5 active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B<sub>5</sub>), pantetheine (and its derivatives) and coenzyme A.

10 Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it  
15 becomes part of the pyruvate dehydrogenase complex and the  $\alpha$ -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-  
20 amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B<sub>12</sub>) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B<sub>12</sub> is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now  
25 known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free  
30 chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B<sub>6</sub>, pantothenate, and biotin. Only Vitamin B<sub>12</sub> is produced solely by fermentation, due to the complexity of

its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

*C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses*

5        Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a  
10        pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA  
15        synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

      Several publications have described the use of these chemicals for these medical  
20        indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or  
25        anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for  
30        chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide

metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

#### *D. Trehalose Metabolism and Uses*

Trehalose consists of two glucose molecules, bound in  $\alpha$ ,  $\alpha$ -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.



## II. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as MP nucleic acid and protein molecules (see Table 1), which play a role in or function in one or more cellular metabolic pathways. In one embodiment, the MP molecules catalyze an enzymatic reaction involving one or more amino acid, *e.g.*, lysine or methionine, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways. In a preferred embodiment, the activity of one or more MP molecules of the present invention, alone or in combination with molecules involved in the same or different metabolic pathway (*e.g.*, methionine or lysine metabolism), in one or more *C. glutamicum* metabolic pathways for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides or trehalose has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the MP molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic pathways in which the MP proteins of the invention are involved are modulated in efficiency or output, which either directly or indirectly modulates the production or efficiency of production of a desired fine chemical by *C. glutamicum*. In a preferred embodiment, the fine chemical is an amino acid, *e.g.*, lysine or methionine. In another preferred embodiment, the MP molecules are metZ, metY, and/or RXA00657 (see Table 1).

The language, "MP protein" or "MP polypeptide" includes proteins which play a role in, *e.g.*, catalyze an enzymatic reaction, in one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathways. Examples of MP proteins include those encoded by the MP genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "MP gene" or "MP nucleic acid sequence" include nucleic acid sequences encoding an MP protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of MP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes

the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

The MP molecules of the present invention may be combined with one or more MP molecules of the invention or one or more molecules of the same or different metabolic pathway to increase the yield of a desired fine chemical. In a preferred embodiment, the fine chemical is an amino acid, *e.g.*, lysine or methionine. Alternatively, or in addition, a byproduct which is not desired may be reduced by combination or disruption of MP molecules or other metabolic molecules (*e.g.*, molecules involved in lysine or methionine metabolism). MP molecules combined with other molecules of the same or a different metabolic pathway may be altered in their nucleotide sequence and in the corresponding amino acid sequence to alter their activity under physiological conditions, which leads to an increase in productivity and/or yield of a desired fine chemical. In a further embodiment, an MP molecule in its original or in its above-described altered form may be combined with other molecules of the same or a different metabolic pathway which are altered in their nucleotide sequence in such a way that their activity is altered under physiological conditions which leads to an increase in productivity and/or yield of a desired fine chemical, *e.g.*, an amino acid such as methionine or lysine.

In another embodiment, the MP molecules of the invention, alone or in combination with one or more molecules of the same or different metabolic pathway, are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. Using recombinant genetic techniques, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, e.g., lysine or methionine, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented.

10 Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of one of these desired fine chemicals may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of other fine chemicals besides the amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Metabolism of any one compound is necessarily intertwined with other biosynthetic and degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway.

20 Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins, may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

30 The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* MP DNAs and the predicted amino acid sequences of the *C.*

*glutamicum* MP proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode metabolic pathway proteins, *e.g.*, proteins involved in the methionine or lysine metabolic pathways.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention (*e.g.*, the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% or more homologous to the selected amino acid sequence.

An MP protein of the invention, or a biologically active portion or fragment thereof, alone or in combination with one or more proteins of the same or different metabolic pathway, can catalyze an enzymatic reaction in one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or have one or more of the activities set forth in Table 1 (*e.g.*, metabolism of methionine or lysine biosynthesis).

Various aspects of the invention are described in further detail in the following subsections:

#### *A. Isolated Nucleic Acid Molecules*

One aspect of the invention pertains to isolated nucleic acid molecules that encode MP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of MP-encoding nucleic acid (*e.g.*, MP DNA). As used herein, the term

"nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (*e.g.*, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* MP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsch, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO of the

Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an MP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing, correspond to the *Corynebacterium glutamicum* MP DNAs of the invention. This DNA comprises sequences encoding MP proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the nucleic acid sequences of the Sequence Listing.

For the purposes of this application, it will be understood that some of the MP nucleic acid and amino acid sequences set forth in the Sequence Listing have an identifying RXA, RXN, RXS, or RXC number having the designation "RXA", "RXN", "RXS", or "RXC" followed by 5 digits (*i.e.*, RXA, RXN, RXS, or RXC). Each of the nucleic acid sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, RXS, or RXC designation to eliminate confusion. The recitation "one of the odd-numbered sequences of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by their

differing RXA, RXN, RXS, or RXC designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence. For example, the coding region for RXA00115 is set forth in SEQ ID NO:69, while the amino acid sequence which it encodes is set forth as SEQ ID NO:70. The sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, RXS, or RXC designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequences designated RXA00115, RXN00403, and RXS03158 are translations of the coding regions of the nucleotide sequences of nucleic acid molecules RXA00115, RXN00403, and RXS03158, respectively. The correspondence between the RXA, RXN, RXS, and RXC nucleotide and amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, RXS, or RXC designation. For example, SEQ ID NO:77, designated, as indicated on Table 1, as "F RXA00254", is an F-designated gene.

Also listed on Table 1 are the *metZ* (or *metY*) and *metC* genes (designated as SEQ ID NO:1 and SEQ ID NO:3, respectively. The corresponding amino acid sequence encoded by the *metZ* and *metC* genes are designated as SEQ ID NO:2 and SEQ ID NO:5, respectively.

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (e.g., a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is sufficiently complementary to one of the nucleotide sequences shown in the Sequence Listing (e.g., the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%,

54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least  
5 about 95%, 96%, 97%, 98%, 99%, 99.7% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a  
10 combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

15 Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MP protein. The nucleotide sequences determined from the cloning of the MP genes from *C. glutamicum* allows for  
20 the generation of probes and primers designed for use in identifying and/or cloning MP homologues in other cell types and organisms, as well as MP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about  
25 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone MP homologues.  
30 Probes based on the MP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-



factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an MP protein, such as by measuring a level of an MP-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting MP mRNA levels or determining whether a genomic MP gene has been mutated or deleted.

5 In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction in an amino acid, vitamin, 10 cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence 15 Listing) amino acid residues to an amino acid sequence of the invention such that the protein or portion thereof is able to catalyze an enzymatic reaction in a *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathway. Protein members of such metabolic pathways, as described herein, function to catalyze the biosynthesis or degradation of one or more of: amino acids, 20 vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose. Examples of such activities are also described herein. Thus, "the function of an MP protein" contributes to the overall functioning of one or more such metabolic pathway and contributes, either directly or indirectly, to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of MP protein activities are set 25 forth in Table 1.

In another embodiment, the protein is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 30 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the MP nucleic acid molecules of the invention are preferably biologically active portions of one of the MP proteins. As used herein, the term "biologically active portion of an MP protein" is intended to include a portion, e.g., a domain/motif, of an MP protein that catalyzes an enzymatic reaction in one or more *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or has an activity as set forth in Table 1. To determine whether an MP protein or a biologically active portion thereof can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an MP protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the MP protein or peptide (e.g., by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (e.g., a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same MP protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (e.g., an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Table 2, which was available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the

invention which is greater than that of a sequence of the prior art (e.g., a Genbank sequence (or the protein encoded by such a sequence) set forth in Table 2). For example, the invention includes a nucleotide sequence which is greater than and/or at least 45% identical to the nucleotide sequence designated RXA00657 SEQ ID NO:5

- 5 One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino
- 10 acid sequences having percent identities greater than the lower threshold so calculated (e.g., at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%,
- 15 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% or more identical) are also encompassed by the invention.

- In addition to the *C. glutamicum* MP nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by one of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the
- 20 amino acid sequences of MP proteins may exist within a population (e.g., the *C. glutamicum* population). Such genetic polymorphism in the MP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MP protein, preferably a *C. glutamicum* MP protein. Such
- 25 natural variations can typically result in 1-5% variance in the nucleotide sequence of the MP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in MP that are the result of natural variation and that do not alter the functional activity of MP proteins are intended to be within the scope of the invention.

- Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum*
- 30 homologues of the *C. glutamicum* MP DNA of the invention can be isolated based on their homology to the *C. glutamicum* MP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in

another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or  
5 more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about  
10 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to one of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by  
15 one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*,  
20 encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* MP protein.

In addition to naturally-occurring variants of the MP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the invention, thereby leading to  
25 changes in the amino acid sequence of the encoded MP protein, without altering the functional ability of the MP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the MP proteins (*e.g.*, an even-  
30 numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said MP protein, whereas an "essential" amino acid residue is required for MP protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-

conserved in the domain having MP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MP proteins that contain changes in amino acid residues that are not essential for MP activity. Such MP proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the MP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the invention and is capable of catalyzing an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the amino acid sequences of the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an MP protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of

the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MP protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MP activity described herein to identify mutants that retain MP activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding MP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire MP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is

antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO.:1 (*metZ*) comprises nucleotides 363 to 1673). In another  
 5 embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding MP disclosed herein (*e.g.*, the  
 10 sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MP mRNA. For  
 15 example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an  
 20 antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified  
 25 nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine,  
 30 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine,

uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MP protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-*o*-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes



(described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave MP mRNA transcripts to thereby inhibit translation of MP mRNA. A ribozyme having specificity for an MP-encoding nucleic acid can be designed based upon the nucleotide sequence of an MP DNA disclosed herein (*i.e.*, SEQ ID NO:1

- 5 (*metZ*). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MP-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, MP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of
- 10 RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

- Alternatively, MP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MP nucleotide sequence (*e.g.*, an MP promoter and/or enhancers) to form triple helical structures that prevent transcription of an MP gene in target cells. See generally, Helene, C. (1991) *Anticancer*
- 15 *Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

- Another aspect of the invention pertains to combinations of genes involved in methionine and/or lysine metabolism and the use of to combinations of genes involved in methionine and/or lysine metabolism in the methods of the invention. Preferred
- 20 combinations are the combination of *metZ* with *metC*, *metB* (encoding Cystathionine-Synthase), *metA* (encoding homoserine-O-acetyltransferase), *metE* (encoding Methionine Synthase), *metH* (encoding Methionine Synthase), *hom* (encoding homoserine dehydrogenase), *asd* (encoding aspartatesemialdehyd dehydrogenase), *lysC* /*ask* (encoding aspartokinase) and rxa00657 (herein designated as SEQ ID NO.:5),
- 25 *dapA*, (gene encoding DIHYDRODIPICOLINATE SYNTHASE), *dapB* (gene encoding DIHYDRODIPICOLINATE REDUCTASE), *dapC* (gene encoding 2,3,4,5-tetrahydropyridine-2-carboxylate N—succinyltransferase), *dapD/argD* (gene encoding acetylornithine transaminase), *dapE* (gene encoding succinyldiaminopimelate desuccinylase), *dapF* (gene encoding diaminopimelate epimerase), *lysA* (gene encoding
- 30 diaminopimelate decarboxylase), *ddh* (gene encoding diaminopimelate dehydrogenase), *lysE* (gene encoding for the lysine exporter), *lysG* (gene encoding for the exporter regulator), *hsk* (gene encoding homoserine kinase) as well as genes involved in anaplerotic reaction such as *ppc* (gene encoding phosphoenolpyruvate carboxylase),

*ppcK* (gene encoding phosphoenolpyruvate carboxykinase), *pycA* (gene encoding pyruvate carboxylase), *accD*, *accA*, *accB*, *accC* (genes encoding for subunits of acetyl-CoA-carboxylase), as well as genes of the pentose-phosphate pathway, *gpdh* genes encoding glucose-6-phosphate-dehydrogenase, *opcA*, *pgdh* (gene encoding 6-phosphogluconate-dehydrogenase), *ta* (gene encoding transaldolase), *tk* (gene encoding gene encoding transketolase), *pgl* (gene encoding 6-PHOSPHOGLUCONOLACTONASE), *rlpe* (gene encoding RIBULOSE-PHOSPHATE 3-EPIMERASE) *rpe* (gene encoding RIBOSE 5-PHOSPHATE EPIMERASE) or combinations of the above-mentioned genes of the pentose-phosphate-pathways, or other MP genes of the invention.

The genes may be altered in their nucleotide sequence and in the corresponding amino acid sequence resulting in derivatives in such a way that their activity is altered under physiological conditions which leads to an increase in productivity and/or yield of a desired fine chemical, e.g., an amino acid such as methionine or lysine. One class of such alterations or derivatives is well known for the nucleotide sequence of the *ask* gene encoding aspartokinase. These alterations lead to removal of feed back inhibition by the amino acids lysine and threonine and subsequently to lysine overproduction. In a preferred embodiment the *metZ* gene or altered forms of the *metZ* gene are used in a *Corynebacterium* strain in combination with *ask*, *hom*, *metA* and *metH* or derivatives of these genes. In another preferred embodiment *metZ* or altered forms of the *metZ* gene are used in a *Corynebacterium* strain in combination with *ask*, *hom*, *metA* and *metE* or derivatives of these genes. In a more preferred embodiment, the gene combinations *metZ* or altered forms of the *metZ* gene are combined with *ask*, *hom*, *metA* and *metH* or derivatives of these genes, or *metZ* is combined with *ask*, *hom*, *metA* and *metE* or derivatives of these genes in a *Corynebacterium* strain and sulfur sources such as sulfates, thiosulfates, sulfites and also more reduced sulfur sources such as H<sub>2</sub>S and sulfides and derivatives are used in the growth medium. Also, sulfur sources such as methyl mercaptan, methanesulfonic acid, thioglycolates, thiocyanates, thiourea, sulfur containing amino acids such as cysteine and other sulfur containing compounds can be used. Another aspect of the invention pertains to the use of the above mentioned gene combinations in a *Corynebacterium* strain which is, before or after introduction of the genes, mutagenized by radiation or by mutagenic chemicals well-known to one of ordinary skill in the art and selected for resistance against high concentrations of the fine

chemical of interest, e.g. lysine or methionine or analogues of the desired fine chemical such as the methionine analogues ethionine, methyl methionine, or others. In another embodiment, the gene combinations mentioned above can be expressed in a *Corynebacterium* strain having particular gene disruptions. Preferred are gene  
5 disruptions that encode proteins that favor carbon flux to undesired metabolites. Where methionine is the desired fine chemical the formation of lysine may be unfavorable. In such a case the combination of the above mentioned genes should proceed in a *Corynebacterium* strain bearing a gene disruption of the *lysA* gene (encoding diaminopimelate decarboxylase) or the *ddh* gene (encoding the meso-diaminopimelate  
10 dehydrogenase catalysing the conversion of tetrahydropicolinate to meso-diaminopimelate). In a preferred embodiment, a favorable combination of the above-mentioned genes are all altered in such a way that their gene products are not feed back inhibited by end products or metabolites of the biosynthetic pathway leading to the desired fine chemical. In the case that the desired fine chemical is methionine, the gene  
15 combinations may be expressed in a strain previously treated with mutagenic agents or radiation and selected for the above-mentioned resistance. Additionally, the strain should be grown in a growth medium containing one or more of the above mentioned sulfur sources.

In another embodiment of the invention, a gene was identified from the genome  
20 of *Corynebacterium glutamicum* as a gene coding for a hypothetical transcriptional regulatory protein. This gene is described as RXA00657. The nucleotide sequence of RXA00657 corresponds to SEQ ID NO:5. The amino acid sequence of RXA00657 corresponds to SEQ ID NO:6. It was found that when the RXA00657 gene, as well as upstream and downstream regulatory regions described in the examples, was cloned into  
25 a vector capable of replicating in *Corynebacterium glutamicum* and transformed and expressed in a lysine producing strain such as ATCC13286, that this strain produced more lysine compared to the strain transformed with the same plasmid lacking the aforementioned nucleotide fragment RXA00657. In addition to the observation that the lysine titer was increased in the mentioned strain, the selectivity determined by the  
30 molar amount of lysine produced compared to the molar amount of sucrose consumed was increased (see Example 14). Overexpression of RXA00657 in combination with the overexpression of other genes either directly involved in the lysine specific pathway

such as *lysC*, *dapA*, *dapB*, *dapC*, *dapD*, *dapF*, *ddh*, *lysE*, *lysG*, and *lysR* results in an increase in the production of lysine compared to RXA00657 alone.

### *B. Recombinant Expression Vectors and Host Cells*

5 Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MP protein (or a portion thereof) or combinations of genes wherein at least one gene encodes for an MP protein. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid",  
10 which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other  
15 vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are  
20 often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

25 The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant  
30 expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory

sequence" is intended to include promoters, repressor binding sites, activator binding sites, enhancers and other expression control elements (*e.g.*, terminators, polyadenylation signals, or other elements of mRNA secondary structure). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression*

5 *Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990).

Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI<sup>q</sup>*-, *T7*-, *T5*-, *T3*-,  
10 *gal*-, *trc*-, *ara*-, *SP6*-, *amy*, *SPO2*,  $\lambda$ -*P<sub>R</sub>*- or  $\lambda$  *P<sub>L</sub>*, which are used preferably in bacteria.

Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as *ADC1*, *MF $\alpha$* , *AC*, *P-60*, *CYC1*, *GAPDH*, *TEF*, *rp28*, *ADH*, promoters from plants such as *CaMV/35S*, *SSU*, *OCS*, *lib4*, *usp*, *STLS1*, *B33*, *nos* or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of

15 ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, MP proteins, mutant forms of MP proteins,  
20 fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of MP proteins in prokaryotic or eukaryotic cells. For example, MP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992)

25 "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge),  
30 algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells.

Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

- 5           Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically  
10   serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion  
15   moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

- Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase  
20   (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the MP protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin.  
25   Recombinant MP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

- Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-  
30   III113-B1,  $\lambda$ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase

transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident  $\lambda$  prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), , 2  $\mu$ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: *Applied Molecular Genetics of Fungi*, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York (ISBN 0 444 904018).

Alternatively, the MP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of

proteins in cultured insect cells (e.g., Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the MP proteins of the invention may be expressed in  
5 unicellular plant cells (such as algae) or in plant cells from higher plants (e.g., the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for  
10 plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian  
15 expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both  
20 prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.*

In another embodiment, the recombinant mammalian expression vector is  
25 capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988)  
30 *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddie (1989) *PNAS* 86:5473-5477),



pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the  $\alpha$ -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to MP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those of ordinary skill in the art. Microorganisms

related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an MP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an MP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MP gene. Preferably, this MP gene is a *Corynebacterium glutamicum* MP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous MP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively,

the vector can be designed such that, upon homologous recombination, the endogenous MP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous MP protein). In the homologous recombination vector, the altered portion  
5 of the MP gene is flanked at its 5' and 3' ends by additional nucleic acid of the MP gene to allow for homologous recombination to occur between the exogenous MP gene carried by the vector and an endogenous MP gene in a microorganism. The additional flanking MP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA  
10 (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) *Cell* 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced MP gene has homologously recombined with the endogenous MP gene are selected, using art-known techniques.

15 In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an MP gene on a vector placing it under control of the lac operon permits expression of the MP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

20 In another embodiment, an endogenous MP gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced MP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MP protein. In still another  
25 embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described MP gene and protein modifications may be readily  
30 produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an MP protein. Accordingly, the invention

further provides methods for producing MP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an MP protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MP protein) in a suitable medium until MP protein is produced. In another embodiment, the method further comprises isolating MP proteins from the medium or the host cell.

### *C. Isolated MP Proteins*

Another aspect of the invention pertains to isolated MP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of MP protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of MP protein having less than about 30% (by dry weight) of non-MP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-MP protein, still more preferably less than about 10% of non-MP protein, and most preferably less than about 5% non-MP protein. When the MP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of MP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of MP protein having less than about 30% (by dry weight) of chemical precursors or non-MP chemicals, more preferably less than about 20% chemical precursors or non-MP chemicals, still more preferably less than about 10% chemical precursors or non-MP chemicals, and most preferably less than about 5% chemical precursors or non-MP chemicals. In preferred embodiments, isolated proteins or

biologically active portions thereof lack contaminating proteins from the same organism from which the MP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MP protein in a microorganism such as *C. glutamicum*.

5 An isolated MP protein or a portion thereof of the invention can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the  
10 invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an MP protein of  
15 the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the MP protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another  
20 preferred embodiment, the MP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or  
25 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a  
30 combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred MP proteins of the present invention also preferably possess at least one of the MP activities described herein. For example, a preferred MP protein of the present invention includes an amino acid sequence encoded by a

nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention, and which can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or which has one or more of the activities set forth in Table 1.

5 In other embodiments, the MP protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in  
10 another embodiment, the MP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or  
15 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% or more homologous to an entire amino acid sequence of the invention and which has at least one of the MP activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of  
20 identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention.

Biologically active portions of an MP protein include peptides comprising amino  
25 acid sequences derived from the amino acid sequence of an MP protein, *e.g.*, an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an MP protein, which include fewer amino acids than a full length MP protein or the full length protein which is homologous to an MP protein, and exhibit at least one activity of an MP protein. Typically, biologically  
30 active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an MP protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant

techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MP protein include one or more selected domains/motifs or portions thereof having biological activity.

MP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the MP protein is expressed in the host cell. The MP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MP protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-MP antibody, which can be produced by standard techniques utilizing an MP protein or fragment thereof of this invention.

The invention also provides MP chimeric or fusion proteins. As used herein, an MP "chimeric protein" or "fusion protein" comprises an MP polypeptide operatively linked to a non-MP polypeptide. An "MP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to MP, whereas a "non-MP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MP protein, *e.g.*, a protein which is different from the MP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the MP polypeptide and the non-MP polypeptide are fused in-frame to each other. The non-MP polypeptide can be fused to the N-terminus or C-terminus of the MP polypeptide. For example, in one embodiment the fusion protein is a GST-MP fusion protein in which the MP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant MP proteins. In another embodiment, the fusion protein is an MP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an MP protein can be increased through use of a heterologous signal sequence.

Preferably, an MP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended

termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

- 5 Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially  
10 available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An MP-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MP protein.

- Homologues of the MP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the MP protein. As used herein, the term "homologue"  
15 refers to a variant form of the MP protein which acts as an agonist or antagonist of the activity of the MP protein. An agonist of the MP protein can retain substantially the same, or a subset, of the biological activities of the MP protein. An antagonist of the MP protein can inhibit one or more of the activities of the naturally occurring form of the MP protein, by, for example, competitively binding to a downstream or upstream  
20 member of the MP cascade which includes the MP protein. Thus, the *C. glutamicum* MP protein and homologues thereof of the present invention may modulate the activity of one or more metabolic pathways in which MP proteins play a role in this microorganism.

- In an alternative embodiment, homologues of the MP protein can be identified  
25 by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the MP protein for MP protein agonist or antagonist activity. In one embodiment, a variegated library of MP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MP variants can be produced by, for example, enzymatically ligating a mixture of synthetic  
30 oligonucleotides into gene sequences such that a degenerate set of potential MP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of MP sequences therein. There are a variety of methods which can be used to produce libraries of potential MP



homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the MP protein coding can be used to generate a variegated population of MP fragments for screening and subsequent selection of homologues of an MP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated MP library, using methods well known in the art.

*D. Uses and Methods of the Invention*

5       The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of MP protein  
10       regions required for function; modulation of an MP protein activity; modulation of the activity of an MP pathway; and modulation of cellular production of a desired compound, such as a fine chemical.

      The MP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a  
15       close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene  
20       which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is not pathogenic to humans, it is related to species which are human pathogens, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this  
25       disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the  
30       disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in the Sequence Listing) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The MP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may

give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the MP nucleic acid molecules of the invention may result in the production of MP proteins having functional differences from the wild-type MP proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention also provides methods for screening molecules which modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more MP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the MP protein is assessed.

When the desired fine chemical to be isolated from large-scale fermentative culture of *C. glutamicum* is an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose, modulation of the activity or efficiency of activity of one or more of the proteins of the invention by recombinant genetic mechanisms may directly impact the production of one of these fine chemicals. For example, in the case of an enzyme in a biosynthetic pathway for a desired amino acid, improvement in efficiency or activity of the enzyme (including the presence of multiple copies of the gene) should lead to an increased production or efficiency of production of that desired amino acid. In the case of an enzyme in a biosynthetic pathway for an amino acid whose synthesis is in competition with the synthesis of a desired amino acid, any decrease in the efficiency or activity of this enzyme (including deletion of the gene) should result in an increase in production or efficiency of production of the desired amino acid, due to decreased competition for intermediate compounds and/or energy. In the case of an enzyme in a degradation pathway for a desired amino acid, any decrease in efficiency or activity of the enzyme should result in a greater yield or efficiency of production of the desired product due to a decrease in its degradation. Lastly, mutagenesis of an enzyme involved in the biosynthesis of a desired amino acid such that this enzyme is no longer is capable of feedback inhibition should result in increased yields or efficiency of production of the desired amino acid. The same should apply to the biosynthetic and

degradative enzymes of the invention involved in the metabolism of vitamins, cofactors, nutraceuticals, nucleotides, nucleosides and trehalose.

Similarly, when the desired fine chemical is not one of the aforementioned compounds, the modulation of activity of one of the proteins of the invention may still  
5 impact the yield and/or efficiency of production of the compound from large-scale culture of *C. glutamicum*. The metabolic pathways of any organism are closely interconnected; the intermediate used by one pathway is often supplied by a different pathway. Enzyme expression and function may be regulated based on the cellular levels of a compound from a different metabolic process, and the cellular levels of molecules  
10 necessary for basic growth, such as amino acids and nucleotides, may critically affect the viability of the microorganism in large-scale culture. Thus, modulation of an amino acid biosynthesis enzyme, for example, such that it is no longer responsive to feedback inhibition or such that it is improved in efficiency or turnover may result in increased cellular levels of one or more amino acids. In turn, this increased pool of amino acids  
15 provides not only an increased supply of molecules necessary for protein synthesis, but also of molecules which are utilized as intermediates and precursors in a number of other biosynthetic pathways. If a particular amino acid had been limiting in the cell, its increased production might increase the ability of the cell to perform numerous other metabolic reactions, as well as enabling the cell to more efficiently produce proteins of  
20 all kinds, possibly increasing the overall growth rate or survival ability of the cell in large scale culture. Increased viability improves the number of cells capable of producing the desired fine chemical in fermentative culture, thereby increasing the yield of this compound. Similar processes are possible by the modulation of activity of a degradative enzyme of the invention such that the enzyme no longer catalyzes, or  
25 catalyzes less efficiently, the degradation of a cellular compound which is important for the biosynthesis of a desired compound, or which will enable the cell to grow and reproduce more efficiently in large-scale culture. It should be emphasized that optimizing the degradative activity or decreasing the biosynthetic activity of certain molecules of the invention may also have a beneficial effect on the production of certain  
30 fine chemicals from *C. glutamicum*. For example, by decreasing the efficiency of activity of a biosynthetic enzyme in a pathway which competes with the biosynthetic pathway of a desired compound for one or more intermediates, more of those intermediates should be available for conversion to the desired product. A similar

situation may call for the improvement of degradative ability or efficiency of one or more proteins of the invention.

This aforementioned list of mutagenesis strategies for MP proteins to result in increased yields of a desired compound is not meant to be limiting; variations on these mutagenesis strategies will be readily apparent to one of ordinary skill in the art. By these mechanisms, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention. Preferred compounds to be produced by *Corynebacterium glutamicum* strains are the amino acids L-lysine and L-methionine.

In one embodiment, the *metC* gene encoding cystathionine  $\beta$ -lyase, the third enzyme in the methionine biosynthetic pathway, was isolated from *Corynebacterium glutamicum*. The translational product of the gene showed no significant homology with that of *metC* gene from other organisms. Introduction of the plasmid containing the *metC* gene into *C. glutamicum* resulted in a 5-fold increase in the activity of cystathionine  $\beta$ -lyase. The protein product, now designated MetC (corresponding to SEQ ID NO:4), which encodes a protein product of 35,574 Daltons and consists of 325 amino acids, is identical to the previously reported *aecD* gene (Rossol, I. and Puhler, A. (1992) *J. Bacteriology* 174, 2968-2977) except the existence of two different amino acids. Like *aecD* gene, when present in multiple copies, *metC* gene conferred resistance to S-( $\beta$ -aminoethyl)-cysteine which is a toxic lysine analog. However, genetic and biochemical evidences suggest that the natural activity of *metC* gene product is to mediate methionine biosynthesis in *C. glutamicum*. Mutant strains of *metC* were constructed and the strains showed methionine prototrophy. The mutant strains completely lost their ability to show resistance to S-( $\gamma$ -aminoethyl)-cysteine. These results show that, in addition to the transsulfuration, which is another biosynthetic pathway, the direct sulfhydrylation pathway is functional in *C. glutamicum* as a parallel biosynthetic route for methionine.

In yet another embodiment, it is also shown that the additional sulfhydrylation pathway is catalyzed by *O*-acetylhomoserine sulfhydrylase. The presence of the pathway is demonstrated by the isolation of the corresponding *metZ* (or *metY*) gene and enzyme (corresponding to SEQ ID NO:1 and SEQ ID NO:2, respectively). Among the eukaryotes, fungi and yeast species have been reported to have both the transsulfuration and direct sulfhydrylation pathway. Thus far, no prokaryotic organism which possesses both pathways has been found. Unlike *E. coli* which only possesses single biosynthetic route for lysine, *C. glutamicum* possesses two parallel biosynthetic pathways for the amino acid. The biosynthetic pathway for methionine in *C. glutamicum* is analogous to that of lysine in that aspect.

The gene *metZ* is located in the upstream region of *metA*, which is the gene encoding the enzyme catalysing the first step of methionine biosynthesis (Park, S.-D., *et al.* (1998) *Mol. Cells* 8, 286-294). Regions upstream and downstream of *metA* were sequenced to identify other *met* genes. It appears that *metZ* and *metA* form an operon. Expression of the genes encoding MetA and MetZ leads to overproduction of the corresponding polypeptides.

Surprisingly, *metZ* clones can complement methionine auxotrophic *Escherichia coli metB* mutant strains. This shows that the protein product of *metZ* catalyzes a step that can bypass the step catalyzed by the protein product of *metB*. *MetZ* was also disrupted and the mutant strain showed methionine prototrophy. *Corynebacterium glutamicum metB* and *metZ* double mutants were also constructed. The double mutant is auxotrophic for methionine. Thus, *metZ* encodes a protein catalysing the reaction from *O*-Acetyl-Homoserine to Homocysteine, which is one step in the sulfhydrylation pathway of methionine biosynthesis. *Corynebacterium glutamicum* contains both the transsulfuration and the sulfhydrylation pathway of methionine biosynthesis.

Introduction of *metZ* into *C. glutamicum* resulted in the expression of a 47,000 Dalton protein. Combined introduction of *metZ* and *metA* in *C. glutamicum* resulted in the appearance of *metA* and *metZ* proteins as shown by gel electrophoresis. If the *Corynebacterium* strain is a lysine overproducer, introduction of a plasmid containing *metZ* and *metA* resulted in a lower lysine titer but accumulation of homocysteine and methionine is detected.

In another embodiment *metZ* and *metA* were introduced into *Corynebacterium glutamicum* strains together with the *hom* gene, encoding the homoserine dehydrogenase, catalysing the conversion from aspartate semialdehyde to homoserine. Different *hom* genes from different organisms were chosen for this experiment. The *Corynebacterium glutamicum* *hom* gene can be used as well as *hom* genes from other procaryotes like *Escherichia coli* or *Bacillus subtilis* or the *hom* gene of eukaryotes such as *Saccharomyces cerevisiae*, *Shizosaccharomyces pombe*, *Ashbya gossypii* or algae, higher plants or animals. It may be that the *hom* gene is insensitive against feed back inhibition mediated by any metabolites that occur in the biosynthetic routes of the amino acids of the aspartate family, like aspartate, lysine, threonine or methionine. Such metabolites are for example aspartate, lysine, methionine, threonine, aspartyl-phosphate, aspartate semialdehyde, homoserine, cystathionine, homocysteine or any other metabolite that occurs in this biosynthetic routes. In addition to the metabolites, the homoserine dehydrogenase may be insensitive against inhibition by analogues of all those metabolites or even against other compounds involved in this metabolism as there are other amino acids like cysteine or cofactors like vitamin B12 and all of its derivatives and S-adenosylmethionine and its metabolites and derivatives and analogues. The insensitivity of the homoserine dehydrogenase against all these, a part of these or only one of these compounds may either be its natural attitude or it may be the result from one or more mutations that resulted from classical mutation and selection using chemicals or irradiation or other mutagens. The mutations could also be introduced into the *hom* gene using gene technology, for example the introduction of site specific point mutations or by any method aforementioned for the MP or MP encoding DNA-sequences.

When a *hom* gene was combined with the *metZ* and *metA* genes and introduced into a *Corynebacterium glutamicum* strain that is a lysine overproducer, lysine accumulation was reduced and homocysteine and methionine accumulation was enhanced. A further enhancement of homocysteine and methionine concentrations can be achieved, if a lysine overproducing *Corynebacterium glutamicum* strain is used and a disruption of the *ddh* gene or the *lysA* gene was introduced prior to the transformation with DNA containing a *hom* gene and *metZ* and *metA* in combination. The overproduction of homocysteine and methionine was possible using different sulfur sources. Sulfates, thiosulfates, sulfites and also more reduced sulfur sources like H<sub>2</sub>S and sulfides and derivatives could be used. Also, organic sulfur sources like methyl mercaptan,



thioglycolates, thiocyanates, thiourea, sulfur containing amino acids like cysteine and other sulfur containing compounds can be used to achieve homocysteine and methionine overproduction.

5 In another embodiment, the *metC* gene was introduced into a *Corynebacterium glutamicum* strain using aforementioned methods. The *metC* gene can be transformed into the strain in combination with other genes like *metB*, *metA* and *metA*. The *hom* gene can also be added. When the *hom* gene, the *met C*, *metA* and *metB* genes were combined on a vector and introduced into a *Corynebacterium glutamicum* strain, homocysteine and methionine overproduction was achieved. The overproduction of homocysteine and  
10 methionine was possible using different sulfur sources. Sulfates, thiosulfates, sulfites and also more reduced sulfur sources like H<sub>2</sub>S and sulfides and derivatives could be used. Also, organic sulfur sources like methyl mercaptan, thioglycolates, thiocyanates, thiourea, sulfur containing amino acids like cysteine and other sulfur containing compounds can be used to achieve homocysteine and methionine overproduction.

15

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

### Exemplification

5

#### **Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC13032**

A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l  $\text{MgSO}_4 \times 7\text{H}_2\text{O}$ , 10 ml/l  $\text{KH}_2\text{PO}_4$  solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l  $(\text{NH}_4)_2\text{SO}_4$ , 1 g/l NaCl, 2 g/l  $\text{MgSO}_4 \times 7\text{H}_2\text{O}$ , 0.2 g/l  $\text{CaCl}_2$ , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l  $\text{FeSO}_4 \times \text{H}_2\text{O}$ , 10 mg/l  $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$ , 3 mg/l  $\text{MnCl}_2 \times 4\text{H}_2\text{O}$ , 30 mg/l  $\text{H}_3\text{BO}_3$ , 20 mg/l  $\text{CoCl}_2 \times 6\text{H}_2\text{O}$ , 1 mg/l  $\text{NiCl}_2 \times 6\text{H}_2\text{O}$ , 3 mg/l  $\text{Na}_2\text{MoO}_4 \times 2\text{H}_2\text{O}$ , 500 mg/l complexing agent (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours.

During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30 min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA  
5 prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

**Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.**

- 10 Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.*, Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)
- 15 Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene library specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).
- 20

For the isolation of *metC* clones, *E. coli* JE6839 cells were transformed with the library DNA and plated onto the M9 minimal medium containing ampicillin and appropriate supplements. The plates were incubated at 37°C for 5 days. Colonies were  
25 isolated and screened for the plasmid content. The complete nucleotide sequence of the isolated *metC* gene was determined by methods well-known to one of ordinary skill in the art.

**Example 3: DNA Sequencing and Computational Functional Analysis**

- 30 Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (*see e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-

512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' (SEQ ID NO:123) or 5'-GTAAAACGACGGCCAGT-3' (SEQ ID NO.:124).

#### 5 Example 4: *In vivo* Mutagenesis

*In vivo* mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (e.g., *mutHLS*, *mutD*, *mutT*, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

#### 15 Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as e.g., pHM1519 or pBL1) which replicate autonomously (for review see, e.g., Martin, J.F. et al. (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. et al. (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which an origin of replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see e.g., Yoshihama, M. et al. (1985) *J. Bacteriol.* 162:591-597,

Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of  
5 *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for  
10 *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which  
15 comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

20 Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through  
25 the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional  
30 terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH: Weinheim.

**Example 6: Assessment of the Expression of the Mutant Protein**

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as SDS-acrylamide gel electrophoresis, were employed. The overproduction of *metC* and *metZ* in combination with *metA* in *Corynebacterium glutamicum* was demonstrated by this method. Western blot may also be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

**Example 7: Growth of Escherichia coli and Genetically Modified Corynebacterium glutamicum — Media and Culture Conditions**

*E. coli* strains are routinely grown in MB and LB broth, respectively (Follettie, M. T., *et al.* (1993) *J. Bacteriol.* 175, 4096-4103). Minimal media for *E. coli* is M9 and modified MCGC (Yoshihama, M., *et al.* (1985) *J. Bacteriol.* 162, 591-507). Glucose was

added to a final concentration of 1%. Antibiotics were added in the following amounts (micrograms per milliliter): ampicillin, 50; kanamycin, 25; nalidixic acid, 25. Amino acids, vitamins, and other supplements were added in the following amounts: methionine, 9.3 mM; arginine, 9.3 mM; histidine, 9.3 mM; thiamine, 0.05 mM. *E. coli* cells were  
5 routinely grown at 37°C, respectively.

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992)  
10 "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as  
15 very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials  
20 which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as  $\text{NH}_4\text{Cl}$  or  $(\text{NH}_4)_2\text{SO}_4$ ,  $\text{NH}_4\text{OH}$ , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

The overproduction of sulfur containing amino acids like homocysteine and  
25 methionine was made possible using different sulfur sources. Sulfates, thiosulfates, sulfites and also more reduced sulfur sources like  $\text{H}_2\text{S}$  and sulfides and derivatives can be used. Also, organic sulfur sources like methyl mercaptan, thioglycolates, thiocyanates, thiourea, sulfur containing amino acids like cysteine and other sulfur containing compounds can be used to achieve homocysteine and methionine overproduction

30 Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating

compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently  
5 originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0  
10 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth,  
15 or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media.  
20 An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH<sub>4</sub>OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex  
25 compounds have high buffer capacities. If a fermentor is utilized for culturing the microorganisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as  
30 microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth



medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

- 5           If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD<sub>600</sub> of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 10 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

#### Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

- 15           The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, 20 applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3<sup>rd</sup> ed. Academic Press: New 25 York; Bisswanger, H., (1994) *Enzymkinetik*, 2<sup>nd</sup> ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3<sup>rd</sup> ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 30 352-363.

Cell extracts from *Corynebacterium glutamicum* were prepared as described previously (Park, S.-D., *et al.* (1998) *Mol. Cells* 8, 286-294). Cystathionine β-lyase was assayed as follows. The assay mixture contained 100 mM Tris-HCl (pH8.5), 0.1 mM

NADH, 1 mM *L*-cystathionine, 5 units of *L*-lactate dehydrogenase, and appropriate amounts of crude extract. Optical changes were monitored at 340 nm. Assay for *S*-( $\alpha$ -aminoethyl)-cysteine (AEC) resistance was carried out as described in Rossol, I. and Pühler, A. (1992) *J. Bacteriol.* 174, 2968-77. The results of cystathionin  $\beta$ -lyase assays  
5 from extracts of different *Corynebacterium glutamicum* strains as well as results of AEC resistance assays of the same strain are summarized in Table 5, below.

Table 5. Expression of cystathionine  $\beta$ -lyase<sup>a</sup>

Strains	Properties	Activity (nmol min <sup>-1</sup> mg <sup>-1</sup> )	Growth on MM <sup>b</sup>	Resistance to AEC <sup>c</sup>
<i>C. glutamicum</i> ASO19E12	-	146	+	+
<i>C. glutamicum</i> ASO19E12/pMT1	Empty vector	145	+	+
<i>C. glutamicum</i> ASO19E12/pSL173	<i>metC</i> clone	797	+	++
<i>C. glutamicum</i> HL457	<i>metC</i> mutant <sup>d</sup>	19	+	-
<i>C. glutamicum</i> HL459	<i>metC</i> mutant <sup>d</sup>	23	+	-
<i>E. coli</i> JE6839	<i>metC</i> mutant	21	-	<u>ND</u> <sup>e</sup>

5 <sup>a</sup> The enzyme was induced by growth to the stationary phase on the minimal medium containing 1% glucose. Cells were harvested, disrupted, and assayed for the activity as described in the Materials and Methods.

<sup>b</sup> MCGC minimal media was used. Growth was monitored on plates.

<sup>c</sup> Cells were grown on plates containing 40 mM S-( $\beta$ -aminoethyl)-cysteine (AEC) for 5 days.

10 <sup>d</sup> The mutants were generated in this study.

<sup>e</sup> Not determined.

The ability of the *metC* clones to express cystathionine  $\beta$ -lyase was tested by enzymatic assay. Crude extracts prepared from the *C. glutamicum* ASO19E12 cells  
 15 harboring plasmid pSL173 were assayed. Cells harboring the plasmid showed approximately a 5-fold increase in the activity of cystathionine  $\beta$ -lyase compared to those harboring the empty vector pMT1 (Table 5), apparently due to the gene-dose effect. SDS-PAGE analysis of crude extracts revealed a putative cystathionine  $\beta$ -lyase band with approximate *M<sub>r</sub>* of 41,000. Intensity of each putative cystathionine  $\beta$ -lyase  
 20 band agreed with the complementation and enzymatic assay data (Table 5). As described above, a region of *metC* appeared to be nearly identical to the previously reported *aecD*. Since the *aecD* gene was isolated on the basis of its ability to confer resistance to S-( $\beta$ -aminoethyl)-cysteine (AEC), a toxic lysine analogue, we tested the protein product of *metC* for the presence of the activity. As shown in Table 5, cells overexpressing  
 25 cystathionine  $\beta$ -lyase showed increased resistance to AEC. The strain carrying a mutation in *metC* gene (see below) completely lost its ability to show a resistant phenotype to AEC.

Assay for O-acetylhomoserine sulphydrylase was performed as follows (Belfaiza, J.,  
 et al. (1998) *J. Bacteriol.* 180, 250-255; Ravanel, S., M. Droux, and R. Douce (1995)  
 30 *Arch. Biochem. Biophys.* 316, 572-584; Foglino, M. (1995) *Microbiology* 141, 431-439).  
 Assay mixture of 0.1 ml contained 20 mM MOPS-NaOH (pH7.5), 10 mM O-

acetylhomoserine, 2 mM Na<sub>2</sub>S in 50 mM NaOH, and an appropriate amount of enzyme. Immediately after the addition of Na<sub>2</sub>S which was added last, the reaction mixture was overlaid with 50 ul of mineral oil. After 30 minute incubation at 30°C, the reaction was stopped by boiling the mixture for 3 minutes. Homocysteine produced in the  
5 reaction was quantified as previously described (Yamagata, S. (1987) *Method Enzymol.* 143, 478-483.). Reaction mixture of 0.1 ml was taken and mixed with 0.1 ml of H<sub>2</sub>O, 0.6 ml of saturated NaCl, 0.1 ml of 1.5 M Na<sub>2</sub>CO<sub>3</sub> containing 67 mM KCN, and 0.1 ml of 2% nitroprusside. After 1 minute incubation at room temperature, optical density was measured at 520 nm. *Corynebacterium* cells harboring additional copies of the *metZ*  
10 gene, e.g., a plasmid containing the *metZ* gene, exhibited significantly higher *metZ* enzyme activities than the same type of *Corynebacterium* cells without additional copies of the *metZ* gene.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays).  
15 The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

20 The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

## 25 **Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product**

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing  
30 the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical

- chromatography such as high performance liquid chromatography (see, for example, Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.*
- 5 (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of
- 10 Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

- In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the
- 15 production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and
- 20 measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

25 **Example 10: Purification of the Desired Product from *C. glutamicum* Culture**

- Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such
- 30 as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotechnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

#### **Example 11: Analysis of the Gene Sequences of the Invention**

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST

programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to MP nucleic acid molecules of the invention. BLAST protein searches can be performed with the  
5 XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the  
10 parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is  
15 part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in  
20 Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology  
25 between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention  
30 were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the

sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

## **Example 12: Construction and Operation of DNA Microarrays**

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizicu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic



acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations

based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

**Example 13: Analysis of the Dynamics of Cellular Protein Populations  
(Proteomics)**

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (e.g., in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (e.g., during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein

precursors (e.g.,  $^{35}\text{S}$ -methionine,  $^{35}\text{S}$ -cysteine,  $^{14}\text{C}$ -labelled amino acids,  $^{15}\text{N}$ -amino acids,  $^{15}\text{NO}_3$  or  $^{15}\text{NH}_4^+$  or  $^{13}\text{C}$ -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, e.g., Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (e.g., different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (e.g., metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

#### **Example 14: Cloning of Genes by Application of the Polymerase Chain Reaction (PCR)**

Genes can be amplified using specific oligonucleotides comprising either nucleotide sequences homologous to sequences of *Corynebacterium glutamicum* or other strains as well as recognition sites of restriction enzymes well known in the art (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A*

- Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). These oligonucleotides can be used to amplify specific DNA-fragments containing parts of the chromosome of mentioned strains using DNA-polymerases such as *T. aquaticus* DNA-polymerase, *P. furiosus* DNA-polymerase, or *P. woesei* DNA-polymerase and dNTPs nucleotides in an appropriate buffer solution as described by the manufacturer.

- Gene fragments such as coding sequences from RXA00657 including appropriate upstream and downstream regions not contained in the coding region of the mentioned gene can be amplified using the aforementioned technologies. Furthermore, these fragments can be purified from unincorporated oligonucleotides and nucleotides. DNA restriction enzymes can be used to produce protruding ends that can be used to ligate DNA fragments to vectors digested with complementary enzymes or compatible enzymes producing ends that can be used to ligate the DNA into the vectors mentioned in Sinsky *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (e.g., *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984). Oligonucleotides used as primers for the amplification of upstream DNA sequence, the coding region sequence and the downstream region of RXA00657 were as follows:

TCGGGTATCCGCGCTACACTTAGA (SEQ ID NO:121);  
GGAAACCGGGGCATCGAACTTA (SEQ ID NO:122).

- Corynebacterium glutamicum* chromosomal DNA with an amount of 200ng was used as a template in a 100µl reaction volume containing 2,5U Pfu Turbo-Polymerase™ (Stratagene™), and 200µM dNTP-nucleotides. The PCR was performed on a PCR-Cycler™ (Perkin Elmer 2400™) using the following temperature/time protocol:
- 1 cycle: 94 °C: 2 min.;  
20 cycle: 94°C : 1 min.;  
52°C: 1 min, 72°C: 1.5 min.,  
1 cycle: 72 °C: 5 min.

Primers were removed from the resulting amplified DNA fragment and the resulting fragment was cloned into the blunt EcoRV site of pBS KS (Stratagene™). The fragment was excised by digestion with the restriction enzymes BamHI/XhoI and ligated

into a BamHI SalI digested vector pB (SEQ ID NO.:125). The resulting vector is called pB RXA00657.

Resulting recombinant vectors can be analyzed using standard techniques described in *e.g.*, Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and can be transferred into *C. glutamicum* using aforementioned techniques.

A *Corynebacterium* strain (ATCC 13286) was treated for a transformation as described. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described, *e.g.*, in Schäfer, A. *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an *Mcr*-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Transformation of a bacterial strain such as *Corynebacterium glutamicum* strain (ATCC 13286) was performed with a plasmid pB containing the aforementioned DNA regions of RXA00657 (SEQ ID NO.:6) and in another case with the vector pB (SEQ ID NO.: ) carrying no additional insertion of nucleic acids.

The resulting strains were plated on and isolated from CM-Medium (10 g/l Glucose 2,5 g/l NaCl, 2,0 g/l Urea, 10 g/l Bacto Peptone (Difco/Becton Dickinson/Sparks USA<sup>TM</sup>), 5 g/l yeast extract (Difco/Becton Dickinson/Sparks USA<sup>TM</sup>), 5g/l meat extract (Difco/Becton Dickinson/Sparks USA<sup>TM</sup>), 22g/l Agar (Difco/Becton Dickinson/Sparks USA<sup>TM</sup>) and 15µg/ml kanamycin sulfate (Serva, Germany) with a adjusted with NaOH to pH of 6.8.

Strains isolated from the aforementioned agar medium were inoculated in 10 ml in a 100ml shake flask containing no baffles in liquid medium containing 100 g/l sucrose 50g/l (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 2,5 g/l NaCl, 2,0 g/l Urea, 10 g/l Bacto Peptone (Difco/Becton Dickinson/Sparks USA), 5 g/l yeast extract (Difco/Becton Dickinson/Sparks USA), 5g/l meat extract (Difco/Becton Dickinson/Sparks USA), and

25g/l CaCO<sub>3</sub> (Riedel de Haen, Germany) . Medium was adjusted with NaOH to pH of 6.8.

Strains were incubated at 30°C for 48h. Supernatants of incubations were prepared by centrifugation 20' at 12,000 rpm in an Eppendorf™ microcentrifuge. Liquid supernatants were diluted and subjected to amino acid analysis (Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein).

The results are shown in Table 6, below.

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Results: Table 6:

Strain ATCC 13286	Plasmid contained	pB	pB RXA00657
lysine produced (g/l)		13.5	14.93
Selectivity (mol lysine/mol consumed Saccharose)		0.235	0.25

### Equivalents

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Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

TABLE 1: Included Genes

## Lysine biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
5	6	RXA00657				AMINOACID BIOSYNTHESIS REGULATOR
7	8	RXA02229	GR00653	2793	3817	DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7)
9	10	RXS02970				ACETYLMORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
11	12	F RXA01009	GR00287	4714	5943	ACETYLMORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
13	14	RXC02390				MEMBRANE SPANNING PROTEIN INVOLVED IN LYSINE METABOLISM
15	16	RXC01798				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN LYSINE METABOLISM
17	18	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
19	20	RXC00657				TRANSCRIPTIONAL REGULATOR INVOLVED IN LYSINE METABOLISM
21	22	RXC00552				CYTOSOLIC PROTEIN INVOLVED IN LYSINE METABOLISM

## Lysine biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
23	24	RXA00534	GR00137	4758	3496	ASPARTOKINASE ALPHA AND BETA SUBUNITS (EC 2.7.2.4)
25	26	RXA00533	GR00137	3469	2438	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC 1.2.1.11)
27	28	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
29	30	RXA02022	GR00613	2063	3169	SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (EC 3.5.1.18)
31	32	RXA00044	GR00007	3458	4393	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
33	34	RXA00863	GR00236	896	1639	DIHYDRODIPICOLINATE REDUCTASE (EC 1.3.1.26)
35	38	RXA00864	GR00236	1694	2443	probable 2,3-dihydrodipicolinate N-C6-lyase (cyclizing) (EC 4.3.3.-) - Corynebacterium glutamicum
37	38	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
39	40	RXN00355	VV0135	31980	30961	MESO-DIAMINOPIMELATE D-DEHYDROGENASE
41	42	F RXA00352	GR00068	861	4	MESO-DIAMINOPIMELATE D-DEHYDROGENASE (EC 1.4.1.16)
43	44	RXA00972	GR00274	3	1379	DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20)
45	46	RXA02653	GR00752	5237	7234	DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20)
47	48	RXA01393	GR00408	4249	3380	LYSINE EXPORT REGULATOR PROTEIN
49	50	RXA00241	GR00036	5443	6945	L-LYSINE TRANSPORT PROTEIN
51	52	RXA01394	GR00408	4320	5018	LYSINE EXPORTER PROTEIN
53	54	RXA00865	GR00236	2647	3549	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function
55	56	RXS02021				2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
57	58	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
59	60	RXC00733				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
61	62	RXC00861				PROTEIN INVOLVED IN LYSINE METABOLISM
63	64	RXC00866				ZN-DEPENDENT HYDROLASE INVOLVED IN LYSINE METABOLISM
65	66	RXC02095				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
67	68	RXC03185				PROTEIN INVOLVED IN LYSINE METABOLISM

Metabolism of methionine and S-adenosyl methionine

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function
1	2	metZ or met				O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10)
3	4	metC				Cystathionine-γ-lyase
69	70	RXA00115	GR00017	5359	4313	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.31)
71	72	RXN00403	VV0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
73	74	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
75	76	RXS03158				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
77	78	F RXA00254	GR00038	2404	1811	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
79	80	RXA02532	GR00726	3085	2039	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
81	82	RXS03159				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
83	84	F RXA02768	GR00770	1919	2521	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
85	86	RXA00216	GR00032	16286	15297	5-methyltetrahydrofolate-homocysteine methyltransferase (methionine synthetase)
87	94	RXA02197	GR00645	4552	4025	5-METHYLTETRAHYDROFOLATE-HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
89	90	RXN02198	VV0302	9228	11726	5-METHYLTETRAHYDROFOLATE-HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
91	91	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE-HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
93	94	RXN03074	VV0042	2238	1741	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)



<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Config.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
95	96	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAGUINONE METHYLTRANSFERASE (EC 2.1.-.-)
97	98	RXN00132	W0124	3612	5045	ADENOSYLMETHIONINE:2-DEMETHYLMENAGUINONE METHYLTRANSFERASE (EC 2.1.-.-)
99	100	F RXA00132	GR00020	7728	7624	ADENOSYLMETHIONINE:2-DEMETHYLMENAGUINONE METHYLTRANSFERASE (EC 2.1.-.-)
101	102	F RXA01371	GR00398	2339	3634	ADENOSYLMETHIONINE:2-DEMETHYLMENAGUINONE METHYLTRANSFERASE (EC 2.1.-.-)
103	104	RXN02085				ADENOSYLMETHIONINE:2-DEMETHYLMENAGUINONE METHYLTRANSFERASE (EC 2.1.-.-)
105	106	F RXA02085	GR00629	3496	5295	ADENOSYLMETHIONINE:2-DEMETHYLMENAGUINONE METHYLTRANSFERASE (EC 2.1.-.-)
107	108	F RXA02086	GR00629	5252	5731	ADENOSYLMETHIONINE:2-DEMETHYLMENAGUINONE METHYLTRANSFERASE (EC 2.1.-.-)
109	110	RXN02648				ADENOSYLMETHIONINE:2-DEMETHYLMENAGUINONE METHYLTRANSFERASE (EC 2.1.-.-)
111	112	F RXA02648	GR00751	5254	4730	ADENOSYLMETHIONINE:2-DEMETHYLMENAGUINONE METHYLTRANSFERASE (EC 2.1.-.-)
113	114	F RXA02658	GR00752	14784	15447	ADENOSYLMETHIONINE:2-DEMETHYLMENAGUINONE METHYLTRANSFERASE (EC 2.1.-.-)
115	116	RXC02238				ADENOSYLMETHIONINE:2-DEMETHYLMENAGUINONE METHYLTRANSFERASE (EC 2.1.-.-)
117	118	RXC00128				ADENOSYLMETHIONINE:2-DEMETHYLMENAGUINONE METHYLTRANSFERASE (EC 2.1.-.-)

### S-2adenosyl methionine (SAM) Biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Config.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
119	120	RXA02240	GR00654	7160	8380	S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6)

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-amino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; flsQ; flsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the flsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; flsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkl	transketolase	
AB024708	glbB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	
AF038651	dciAE; api; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the <i>Corynebacterium glutamicum</i> rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamyolphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in <i>Corynebacterium glutamicum</i> ," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the <i>Corynebacterium glutamicum</i> panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in <i>Escherichia coli</i> ," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ236703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in corynebacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in corynebacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	IlvB, ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dxr	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dxrR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)



GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	acd; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rossol, I. et al. "The Corynebacterium glutamicum acd gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIIM; cgIIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock A TP-binding protein	
U53587	aphA-3	3'5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component I	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	cspI	Psl protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PSI, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PSI is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit

GenBank™ Accession No.	Gene Name	Gene Function	genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Reference
X77384	recA		Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X78491	aceB	Malate synthase	Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X80629	16S rDNA	16S ribosomal RNA	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81379	dapE	Succinyl/diaminopimelate desuccinylase	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X82061	16S rDNA	16S ribosomal RNA	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-36 (1994)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
			Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from C. glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)
X96580	panB; panC; xyIB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-	Sahm, H. et al. "D-pantothenate synthesis in <i>Corynebacterium glutamicum</i> and use of panBC and genes encoding L-valine synthesis for D-pantothenate

GenBank™ Accession No.	Gene Name	alanine ligase; xylulokinase Gene Function	overproduction, "Appl. Environ. Microbiol., 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	<b>Reference</b>
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; fsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of <i>Corynebacterium glutamicum</i> proline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of coryneophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)



GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynebacterium 304L	Moreau, S. et al. "Analysis of the integration functions of $\phi$ phi304L: An integrase module among corynebacteriophages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS, lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dxr	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?, SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)

A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ	
Brevibacterium	ammoniagenes	21054								
Brevibacterium	ammoniagenes	19350								
Brevibacterium	ammoniagenes	19351								
Brevibacterium	ammoniagenes	19352								
Brevibacterium	ammoniagenes	19353								
Brevibacterium	ammoniagenes	19354								
Brevibacterium	ammoniagenes	19355								
Brevibacterium	ammoniagenes	19356								
Brevibacterium	ammoniagenes	21055								
Brevibacterium	ammoniagenes	21077								
Brevibacterium	ammoniagenes	21553								
Brevibacterium	ammoniagenes	21580								
Brevibacterium	ammoniagenes	39101								
Brevibacterium	butanicum	21196								
Brevibacterium	divaricatum	21792	P928							
Brevibacterium	flavum	21474								
Brevibacterium	flavum	21129								
Brevibacterium	flavum	21518								
Brevibacterium	flavum			B11474						
Brevibacterium	flavum			B11472						
Brevibacterium	flavum	21127								
Brevibacterium	flavum	21128								
Brevibacterium	flavum	21427								
Brevibacterium	flavum	21475								
Brevibacterium	flavum	21517								
Brevibacterium	flavum	21528								
Brevibacterium	flavum	21529								
Brevibacterium	flavum			B11477						
Brevibacterium	flavum			B11478						
Brevibacterium	flavum	21127								
Brevibacterium	flavum			B11474						
Brevibacterium	healii	15527								
Brevibacterium	ketoglutamicum	21004								
Brevibacterium	ketoglutamicum	21089								
Brevibacterium	ketosoreductum	21914								
Brevibacterium	lactofermentum				70					
Brevibacterium	lactofermentum				74					
Brevibacterium	lactofermentum				77					
Brevibacterium	lactofermentum	21798								
Brevibacterium	lactofermentum	21799								
Brevibacterium	lactofermentum	21800								
Brevibacterium	lactofermentum	21801								
Brevibacterium	lactofermentum			B11470						
Brevibacterium	lact fermentum			B11471						

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ	
Brevibacterium	lactofermentum	21086								
Brevibacterium	lactofermentum	21420								
Brevibacterium	lactofermentum	21086								
Brevibacterium	lactofermentum	31269								
Brevibacterium	linens	9174								
Brevibacterium	linens	19391								
Brevibacterium	linens	8377								
Brevibacterium	paraffinolyticum					11160				
Brevibacterium	spec.						717.73			
Brevibacterium	spec.						717.73			
Brevibacterium	spec.	14604								
Brevibacterium	spec.	21860								
Brevibacterium	spec.	21864								
Brevibacterium	spec.	21865								
Brevibacterium	spec.	21866								
Brevibacterium	spec.	19240								
Corynebacterium	acetoacidophilum	21476								
Corynebacterium	acetoacidophilum	13870								
Corynebacterium	acetoglutamicum			B11473						
Corynebacterium	acetoglutamicum			B11475						
Corynebacterium	acetoglutamicum	15806								
Corynebacterium	acetoglutamicum	21491								
Corynebacterium	acetoglutamicum	31270								
Corynebacterium	acetophilum			B3671						
Corynebacterium	ammoniagenes	6872						2399		
Corynebacterium	ammoniagenes	15511								
Corynebacterium	fujikense	21496								
Corynebacterium	glutamicum	14067								
Corynebacterium	glutamicum	39137								
Corynebacterium	glutamicum	21254								
Corynebacterium	glutamicum	21255								
Corynebacterium	glutamicum	31830								
Corynebacterium	glutamicum	13032								
Corynebacterium	glutamicum	14305								
Corynebacterium	glutamicum	15455								
Corynebacterium	glutamicum	13058								
Corynebacterium	glutamicum	13059								
Corynebacterium	glutamicum	13060								
Corynebacterium	glutamicum	21492								
Corynebacterium	glutamicum	21513								
Corynebacterium	glutamicum	21526								
Corynebacterium	glutamicum	21543								
Corynebacterium	glutamicum	13287								
Corynebacterium	glutamicum	21851								
Corynebacterium	glutamicum	21253								
Corynebacterium	glutamicum	21514								
Corynebacterium	glutamicum	21516								
Corynebacterium	glutamicum	21299								

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ	
Corynebacterium	glutamicum	21300								
Corynebacterium	glutamicum	39684								
Corynebacterium	glutamicum	21488								
Corynebacterium	glutamicum	21649								
Corynebacterium	glutamicum	21650								
Corynebacterium	glutamicum	19223								
Corynebacterium	glutamicum	13869								
Corynebacterium	glutamicum	21157								
Corynebacterium	glutamicum	21158								
Corynebacterium	glutamicum	21159								
Corynebacterium	glutamicum	21355								
Corynebacterium	glutamicum	31808								
Corynebacterium	glutamicum	21674								
Corynebacterium	glutamicum	21562								
Corynebacterium	glutamicum	21563								
Corynebacterium	glutamicum	21564								
Corynebacterium	glutamicum	21565								
Corynebacterium	glutamicum	21566								
Corynebacterium	glutamicum	21567								
Corynebacterium	glutamicum	21568								
Corynebacterium	glutamicum	21569								
Corynebacterium	glutamicum	21570								
Corynebacterium	glutamicum	21571								
Corynebacterium	glutamicum	21572								
Corynebacterium	glutamicum	21573								
Corynebacterium	glutamicum	21579								
Corynebacterium	glutamicum	19049								
Corynebacterium	glutamicum	19050								
Corynebacterium	glutamicum	19051								
Corynebacterium	glutamicum	19052								
Corynebacterium	glutamicum	19053								
Corynebacterium	glutamicum	19054								
Corynebacterium	glutamicum	19055								
Corynebacterium	glutamicum	19056								
Corynebacterium	glutamicum	19057								
Corynebacterium	glutamicum	19058								
Corynebacterium	glutamicum	19059								
Corynebacterium	glutamicum	19060								
Corynebacterium	glutamicum	19185								
Corynebacterium	glutamicum	13286								
Corynebacterium	glutamicum	21515								
Corynebacterium	glutamicum	21527								
Corynebacterium	glutamicum	21544								
Corynebacterium	glutamicum	21492								
Corynebacterium	glutamicum			B8183						
Corynebacterium	glutamicum			B8182						
Corynebacterium	glutamicum			B12416						
Corynebacterium	glutamicum			B12417						

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ	Other origin
Corynebacterium	glutamicum			B12418						
Corynebacterium	glutamicum			B11476						
Corynebacterium	glutamicum	21608								
Corynebacterium	lilium		P973							
Corynebacterium	nitrilophilus	21419				11594				
Corynebacterium	spec.		P4445							
Corynebacterium	spec.		P4446							
Corynebacterium	spec.	31088								
Corynebacterium	spec.	31089								
Corynebacterium	spec.	31090								
Corynebacterium	spec.	31090								
Corynebacterium	spec.	31090								
Corynebacterium	spec.	15954							20145	
Corynebacterium	spec.	21857								
Corynebacterium	spec.	21862								
Corynebacterium	spec.	21863								
Corynebacterium	Glutamicum*									ASO19
Corynebacterium	Glutamicum**									ASO19 E12
Corynebacterium	Glutamicum***									HL457
Corynebacterium	Glutamicum****									HL459

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4<sup>th</sup> edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

\* Spontaneous rifampin-resistant mutant of *C. glutamicum* ATCC13059<sup>a</sup> Yoshihama et al., 1985

\*\* Restriction-deficient variant of ASO19 Follett et al., 1993

\*\*\* *metC*-disrupted mutant of ASO19E12 This study

\*\*\*\* *metC*-disrupted mutant of ASO19E12 This study

TABLE 4: ALIGNMENT RESULTS

ID #	length (nt)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx000857	908	GB_BA1:AF064700	3481	AF064700	Rhodococcus sp. NO-1 CprS and CprR genes, complete cds.	Rhodococcus sp	40,285	15-Jul-98
met2	1314	GB_BA2:MTV016	53882	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/182.	Mycobacterium tuberculosis	81,278	23-Jun-98
metc	978	GB_BA2:CORCSLYS	2821	M89931	Corynebacterium glutamicum beta C-S lyase (aecD) and branched-chain amino acid uptake	Corynebacterium glutamicum	89,591	04-JUN-1998
rx000023	3579	GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	28-Jun-99
		GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	28-Jun-99
rx000044	1059	EM_PAT:E11760	6911	E11760	Base sequence of sucrose gene.	Corynebacterium glutamicum	42,979	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:126124	6911	126124	Sequence 4 from patent US 5556776.	Unknown.	42,979	07-OCT-1986
		GB_BA2:ECOLW89	178195	U00008	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	39,097	17-DEC-1993
rx000064	1401	GB_PAT:E16763	2517	E16763	gDNA encoding aspartate transferase (AAT).	Corynebacterium glutamicum	95,429	28-Jul-99
		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02003 (D797) RPCI-98 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 113 unordered pieces.	Drosophila melanogaster	31,111	2-Aug-99
rx000072		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02003 (D797) RPCI-98 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS 113 unordered pieces.	Drosophila melanogaster	31,111	2-Aug-99
rx001005	798	GB_BA1:MTV002	58414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/182.	Mycobacterium tuberculosis	37,753	17-Jun-98
		GB_BA1:ECU29581	71128	U29581	Escherichia coli K-12 genome; approximately 63 to 64 minutes.	Escherichia coli	35,669	14-Jan-97
		GB_BA2:AE000366	10405	AE000366	Escherichia coli K-12 MG1655 section 256 of 400 of the complete genome.	Escherichia coli	35,669	12-Nov-98
rx001008	579	GB_EST15:AA494237	367	AA494237	ng83/04.s1 NCLCGAP_P18 Homo sapiens cDNA clone IMAGE:941407 similar to SW:DYR_LACCA P00381 DIHYDROFOLATE REDUCTASE.; mRNA sequence.	Homo sapiens	42,896	20-Aug-97
		GB_BA2:AF161327	2021	AF161327	Corynebacterium diphtheriae histidine kinase ChrS (chrS) and response regulator ChrA (chrA) genes, complete cds.	Corynebacterium diphtheriae	40,210	9-Sep-99
		GB_PAT:AR041189	664	AR041189	Sequence 4 from patent US 5811286.	Unknown.	41,176	29-Sep-98
rx001115	1170	GB_PR4:AC007110	148336	AC007110	Homo sapiens chromosome 17, clone HRPK.472_J_18, complete sequence.	Homo sapiens	36,783	30-MAR-1999
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***; 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***; 93 unordered pieces.	Homo sapiens	40,286	2-Sep-98

### **TABLE 4: ALIGNMENT RESULTS**

[illegible]

TABLE 4: ALIGNMENT RESULTS

rx00198	672	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	92,113	13-MAR-1999
		GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	93,702	13-MAR-1999
		GB_EST24:AI232702	528	AI232702	EST229390 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKICF35 3' end, mRNA sequence.	Rattus sp.	34,221	31-Jan-99
rx00216	1113	GB_HTG2:HSDJ850E9	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***, In unordered pieces.	Homo sapiens	37,965	03-DEC-1999
		GB_HTG2:HSDJ850E9	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***, In unordered pieces.	Homo sapiens	37,965	03-DEC-1999
		GB_PR2:CNS01DSA	159400	AL121766	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-412H8 of RPC1-11 library from chromosome 14 of Homo sapiens (Human), complete sequence.	Homo sapiens	38,788	11-Nov-99
rx00219	1065	GB_HTG2:AC005079_0	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
		GB_HTG2:AC005079_1	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
		GB_HTG2:AC005079_1	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
rx00223	1212	GB_BA1:PPEA3NIF	19771	X98984	Plasmid pEA3 nitrogen fixation genes.	Enterobacter agglomerans	48,828	2-Aug-98
		GB_BA2:AF128444	2477	AF128444	Rhodobacter capsulatus molybdenum cofactor biosynthetic gene cluster, partial sequence.	Rhodobacter capsulatus	40,135	22-MAR-1999
		GB_HTG4:AC010111	138938	AC010111	Drosophila melanogaster chromosome 3L70C1 clone RPC198-9B18, *** SEQUENCING IN PROGRESS ***, 64 unordered pieces.	Drosophila melanogaster	39,527	16-OCT-1999
rx00229	803	GB_BA2:AF124518	1758	AF124518	Corynebacterium glutamicum 3-dehydroquinase (aroD) and shikimate dehydrogenase (aroE) genes, complete cds.	Corynebacterium glutamicum	98,237	18-MAY-1999
		GB_PR3:AC004593	150221	AC004593	Homo sapiens PAC clone DJ0984C11 from 7p14-p15, complete sequence.	Homo sapiens	38,816	18-Apr-98
		GB_HTG2:AC008907	188972	AC008907	Caenorhabditis elegans clone Y76B12, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	Caenorhabditis elegans	37,095	28-Feb-99
rx00241	1626	GB_BA1:CGLYSI	4232	X60312	C. glutamicum lysI gene for L-lysine permease.	Corynebacterium glutamicum	100,000	30-Jan-92
		GB_HTG1:PFMAL13P1	192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, In unordered pieces.	Plasmodium falciparum	34,947	11-Aug-99
		GB_HTG1:PFMAL13P1	192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, In unordered pieces.	Plasmodium falciparum	34,947	11-Aug-99
rx00282	1187	GB_IN2:EHU89855	3219	U89855	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	Entamoeba histolytica	36,498	23-MAY-1997
		GB_IN2:EHU89855	3219	U89855	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	Entamoeba histolytica	37,544	23-MAY-1997
rx00288	531	GB_RO:AF016180	2839	AF016180	Mus musculus connexin-36 (Cx36) gene, complete cds.	Mus musculus	41,858	9-Feb-99
		EM_PAT:E09719	3505	E09719	DNA encoding precursor protein of alkaline cellulase.	Bacillus sp.	34,741	08-OCT-1997 (Rel. 52, Created)
rx00278	1155	GB_PAT:E02133	3494	E02133	gDNA encoding alkaline cellulase.	Bacillus sp.	34,741	29-Sep-97
		GB_IN1:CELK05F8	36912	AF040653	Caenorhabditis elegans cosmid K05F8.	Caenorhabditis elegans	36,943	6-Jan-98



### **TABLE 4: ALIGNMENT RESULTS**

	GB	BA1	CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	9-Apr-97
	GB_RO:	RNU30789	3510	U30789	Rattus norvegicus clone N27 mRNA.	Rattus norvegicus	36,190	20-Aug-96
	GB_BA2:	CGUJ1281	1614	U31281	Corynebacterium glutamicum biotin synthase (bioB) gene, complete cds.	Corynebacterium glutamicum	99,111	21-Nov-86
	GB_BA1:	BRLBI0BA	1647	D14084	Brevibacterium flavum gene for biotin synthetase, complete cds.	Corynebacterium glutamicum	98,489	3-Feb-99
	GB_PAT:	E03937	1005	E03937	DNA sequence encoding Brevibacterium flavum biotin-synthase.	Corynebacterium glutamicum	98,207	29-Sep-97
	GB_BA1:	MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	35,615	24-Jun-99
	GB_BA1:	MSGB32CS	36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	60,917	15-Jun-86
	GB_BA1:	MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	44,606	24-Jun-99
	GB_BA1:	MSGB32CS	36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	52,516	15-Jun-96
	GB_BA1:	MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	38,079	24-Jun-99
	GB_OM:	BOVELA	3242	J02717	Bovine elastin A mRNA, complete cds.	Bos taurus	39,351	27-Apr-93
	GB_BA1:	CGTHRC	3120	X56037	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2).	Corynebacterium glutamicum	99,808	17-Jun-97
	GB_PAT:	I09078	3146	I09078	Sequence 4 from Patent WO 8809819.	Unknown.	99,617	02-DEC-1994
	GB_BA1:	BLTHRESYN	1892	Z29563	Brevibacterium lactofermentum; ATCC 13869;; DNA (genomic);.	Corynebacterium glutamicum	99,170	20-Sep-95
	GB_BA1:	CGGLNA	3686	Y13221	Corynebacterium glutamicum glnA gene.	Corynebacterium glutamicum	100,000	28-Aug-97
	GB_BA2:	AF005635	1690	AF005635	Corynebacterium glutamicum glutamine synthetase (glnA) gene, complete cds.	Corynebacterium glutamicum	98,906	14-Jun-99
	GB_BA1:	MSGB27CS	38793	L78817	Mycobacterium leprae cosmid B27 DNA sequence.	Mycobacterium leprae	66,345	15-Jun-96
	GB_EST27:	A1455217	624	A1455217	LD21828.3prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD21828 3prime, mRNA sequence.	Drosophila melanogaster	34,510	09-MAR-1999
	GB_BA2:	SSU30252	2891	U30252	Synechococcus PCC7942 nucleoside diphosphate kinase and ORF2 protein genes, complete cds, ORF1 protein gene, partial cds, and neutral site I for vector use.	Synechococcus PCC7942	37,084	29-OCT-1999
	GB_EST21:	AA911262	581	AA911262	oe75a02.s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1417418 3' similar to gb:A18757 UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR, GPI-ANCHORED (HUMAN);; mRNA sequence.	Homo sapiens	37,500	21-Apr-98
	GB_BA1:	MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	52,972	09-MAR-1995
	GB_IN2:	AC004373	72722	AC004373	Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.	Drosophila melanogaster	46,341	17-Jul-98
	GB_IN2:	AF145653	3197	AF145653	Drosophila melanogaster clone GH08860 BcDNA.GH08860 (BcDNA.GH08860) mRNA, complete cds.	Drosophila melanogaster	49,471	14-Jun-99
	GB_BA1:	AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	96,556	13-MAR-1999
	GB_BA1:	MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	39,496	17-Jun-98
	GB_BA1:	SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,946	16-Aug-99
	GB_BA1:	AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,374	13-MAR-1999
	GB_BA1:	MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	41,333	17-Jun-98
	GB_BA1:	SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,554	16-Aug-99

TABLE 4: ALIGNMENT RESULTS

rx000387	4853	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,312	13-MAR-1999
		GB_BA1:MTCY1A8	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	36,971	17-Jun-98
		GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,905	18-Aug-99
rx000371	1917	GB_Vi:SBVORFS	7568	M89923	Sugarcane bacilliform virus ORF 1,2 and 3 DNA, complete cds.	Sugarcane bacilliform virus	35,843	12-Jun-93
		GB_EST37:AI987505	380	AI987505	Ljimpes03-215-c10 Ljimp Lambda HybZap two-hybrid library Lotus japonicus cDNA clone LP215-03-c10 5' similar to 60S ribosomal protein L39, mRNA sequence.	Lotus japonicus	42,593	24-Aug-99
rx000377	1245	GB_IN1:CELK09H9	37881	AF043700	Caenorhabditis elegans cosmid K09H9.	Caenorhabditis elegans	34,295	22-Jan-98
		GB_BA1:CCU13664	1678	U13664	Caulobacter crescentus uroporphyrinogen decarboxylase homolog (homE) gene, partial cds.	Caulobacter crescentus	36,832	24-MAR-1995
		GB_PL1:AVSDGENE	1299	Y06606	A. nidulans sD gene.	Emerizella nidulans	39,603	17-OCT-1996
		GB_GSS4 AQ730303	483	AQ730303	genomic clone Plac=1081 Cds=7 Rows=6 genomic survey sequence.	Homo sapiens	36,728	15-Jul-99
rx000382	1425	GB_BA1:PAHEML	4444	X82072	P. aeruginosa hem-1 gene.	Pseudomonas aeruginosa	54,175	18-DEC-1995
		GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	61,143	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequences from clone Y224.	Mycobacterium tuberculosis	61,143	03-DEC-1996
rx000383	1467	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	43,981	27-Aug-99
		GB_HTG2:AC008269	167171	AC008269	Homo sapiens chromosome 17 clone hRPK.515_E_23 map 17, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	35,444	10-Jun-99
		GB_HTG2:AC007638	178053	AC007638	Homo sapiens chromosome 17 clone hRPK.515_O_17 map 17, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	34,821	22-MAY-1999
rx000391	843	GB_EST38:AW017053	613	AW017053	EST272398 Schistosoma mansoni male, Phil LoVerde/Joë Mairick	Schistosoma mansoni	40,472	10-Sep-99
		GB_PAT:AR065852	32207	AR065852	Schistosoma mansoni cDNA clone SMMAS14 5' end, mRNA sequence.	Unknown.	38,586	29-Sep-99
		GB_Vi:AF148805	28559	AF148805	Sequence 20 from patent US 5849564.	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds.	38,509	2-Aug-99
rx000393	1017	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	36,308	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequences from clone Y224.	Mycobacterium tuberculosis	39,282	03-DEC-1996
		GB_BA1:MLB1306	7762	Y13803	Mycobacterium leprae cosmid B1306 DNA.	Mycobacterium leprae	39,228	24-Jun-97
rx000402	623	GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (melA) gene, complete cds.	Corynebacterium glutamicum	98,672	19-MAR-1998
		GB_BA2:AF109162	4514	AF109162	Corynebacterium diphtheriae hemE uptake locus, complete sequence.	Corynebacterium diphtheriae	40,830	8-Jun-99
		GB_BA2:AF082818	20758	AF082818	Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.	Pseudomonas alcaligenes	50,161	08-DEC-1998
rx000403	1254	GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (melA) gene, complete cds.	Corynebacterium glutamicum	99,920	19-MAR-1998
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	52,898	23-Jun-99
		GB_EST23:AI11288	750	AI11288	SWOVAMCAQ02A05SK Onchocerca volvulus adult male cDNA (SAV98MLW-OvAM) Onchocerca volvulus cDNA clone SWOVAMCAQ02A05 5', mRNA sequence.	Onchocerca volvulus	37,565	31-Aug-98

### TABLE 4: ALIGNMENT RESULTS

txa00405	613	GB_BA1:MTV016 GB_PR4:AC005145	53692 143978	AL021841 AC005145	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. Homo sapiens Xp22-168-169 GSHB-523A23 (Genome Systems Human BAC library) complete sequence.	Mycobacterium tuberculosis Homo sapiens	57,259 34,179	23-Jun-99 08-DEC-1998
txa00420	1587	GR_BA1:MTV016 GB_BA1:MTV13D12 GB_BA1:MSGY126 GB_BA1:MSG071CS GB_BA1:AFAC0BTZ GB_BA1:AFAC0BTZ	53692 37065 37164 37568 2760	AI 021841 Z80343 AD00012 L78821 M65904	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. Mycobacterium tuberculosis H37Rv complete genome; segment 158/162. Mycobacterium tuberculosis sequence from clone y128. Mycobacterium leprae cosmid B971 DNA sequence. A caligenes eutrophus chromosomal transketolase (cbtTc) and phosphoglycerate phosphatase (cbpZc) genes, complete cds. Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 25 unordered pieces. Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 25 unordered pieces. Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.	Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium leprae Ralstonia eutropha Homo sapiens Homo sapiens Homo sapiens	40,169 62,031 81,902 39,651 38,677	23-Jun-99 17-Jun-98 10-DEC-1996 15-Jun-96 27-Jul-94
txa00437	579	GB_HTG4:AC009541 GB_HTG4:AC009541 GB_PR4:AC005951	169583 169583 155450	AC009541 AC009541 AC005951	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 25 unordered pieces. Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 25 unordered pieces. Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.	Homo sapiens Homo sapiens Homo sapiens	36,335 36,335 31,738	12-OCT-1999 12-OCT-1999 18-Nov-98
txa00438	591	GB_BA1:MTV016 GB_PL2:AF167358 GB_HTG3:AC009120	53692 1022 269445	AL021841 AF167358 AC009120	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. Rumex acetosa expansin (EXP3) gene, partial cds. Homo sapiens chromosome 16 clone RPC1-11_484E3, *** SEQUENCING IN PROGRESS ***; 34 unordered pieces.	Mycobacterium tuberculosis Rumex acetosa Homo sapiens	37,088 46,538 43,276	23-Jun-99 17-Aug-99 3-Aug-99
txa00440	582	GB_BA2:SKZ86111	7860	Z86111	Streptomyces lividans rpsP, trmD, rplS, sipX, sipY, sipZ, mutT genes and 4 open reading frames.	Streptomyces lividans	43,080	27-OCT-1999
txa00441	1287	GB_BA1:SC2E1 GB_BA1:SC2E1 GB_PR2:HS173D1	38962 38962 117338	AL023797 AL023797 AL031894	Streptomyces coelicolor cosmid 2E1. Streptomyces coelicolor cosmid 2E1. Human DNA sequence from clone 173D1 on chromosome 1p36.21-36.33. Contains ESTs, STSs and GSSs, complete sequence.	Streptomyces coelicolor Streptomyces coelicolor Homo sapiens	42,931 36,702 38,027	4-Jun-98 4-Jun-98 23-Nov-99
txa00448	987	GB_HTG2:HSDJ719K3 GB_HTG2:HSDJ719K3 GB_BA1:SCD78 GB_HTG4:AC009367	267114 267114 36224 226055	AL109931 AL109931 AL034355 AC009367	Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***; in unordered pieces. Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***; in unordered pieces. Streptomyces coelicolor cosmid D78. Drosophila melanogaster chromosome 3LJ76A2 clone RPC198-48B15, *** SEQUENCING IN PROGRESS ***; 44 unordered pieces. Drosophila melanogaster chromosome 3LJ76A2 clone RPC198-48B15, *** SEQUENCING IN PROGRESS ***; 44 unordered pieces.	Homo sapiens Homo sapiens Streptomyces coelicolor Drosophila melanogaster	34,521 34,521 58,410 34,959	03-DEC-1999 03-DEC-1999 26-Nov-98 16-OCT-1999
txa00448	1143	GB_PR3:AC003670 GB_HTG2:AF029367 GB_HTG2:AF029367	88945 148676 148676	AC003670 AF029367 AF029367	Homo sapiens 12q13.1 PAC RPC11-130F5 (Roswell Park Cancer Institute Human PAC library) complete sequence. Homo sapiens chromosome 12 clone RPC1-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***; 156 unordered pieces. Homo sapiens chromosome 12 clone RPC1-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***; 156 unordered pieces.	Homo sapiens Homo sapiens Homo sapiens	34,959 35,682 31,373	16-OCT-1989 9-Jun-98 18-OCT-1997
txa00448	1143	GB_HTG2:AF029367	148676	AF029367	Homo sapiens chromosome 12 clone RPC1-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***; 156 unordered pieces.	Homo sapiens	31,373	18-OCT-1997

TABLE 4: ALIGNMENT RESULTS

rx00450	424	GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCI-98 02.L.16 map 89E-90A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCI-98 02.L.16 map 89E-90A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_EST35:A1818057	412	A1818057	wk14a08.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE2412278 3' similar to gb:Y00764 UBIQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN); mRNA sequence.	Homo sapiens	35,714	24-Aug-99
rx00461	975	GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	39,308	8-Aug-97
		GB_IN1:DMC86E4	28352	AL021086	Drosophila melanogaster cosmid clone 86E4.	Drosophila melanogaster	37,487	27-Apr-99
		GB_GSS15:AQ640325	467	AQ640325	927P1-2H3, TP 927P1 Trypanosoma brucei genomic clone 927P1-2H3, genomic survey sequence.	Trypanosoma brucei	38,116	8-Jul-99
rx00465								
rx00487	1692	GB_BA1:BAGUAA	3666	Y10499	B.ammonia genes guaA gene.	Corynebacterium ammoniagenes	74,259	8-Jan-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	37,248	01-MAR-1994
rx00488	1641	GB_BA1:MTCV78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	39,725	17-Jun-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	39,451	17-Jun-98
		GB_BA1:SCA10601	4692	AJ010601	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Mycobacterium leprae	39,178	01-MAR-1994
rx00489	1245	GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Streptomyces coelicolor	60,835	17-Sep-98
		GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***. In unordered pieces.	Mycobacterium leprae	38,041	01-MAR-1994
		GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***. In unordered pieces.	Homo sapiens	36,766	03-DEC-1999
rx00533	1155	GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,913	17-Feb-97
		GB_BA1:CGCYSCASD	1591	X82928	C. glutamicum aspartate-semialdehyde dehydrogenase gene.	Corynebacterium glutamicum	99,221	17-Feb-97
rx00534	1386	GB_PAT:A07546	2112	A07546	Recombinant DNA fragment (PstI-XhoI).	synthetic construct	99,391	30-Jul-93
		GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,856	17-Feb-97
		GB_BA1:CORASKD	2857	L16848	Corynebacterium flavum aspartokinase (ask), and aspartate-semialdehyde dehydrogenase (asd) genes, complete cds.	Corynebacterium flavesces	88,701	11-Jun-93
rx00538	1494	GB_PAT:E14514	1643	E14514	DNA encoding Brevibacterium aspartokinase.	Corynebacterium glutamicum	98,773	28-Jul-99
		GB_BA1:CGLEUA	3492	X70959	C. glutamicum gene leuA for isopropylmalate synthase.	Corynebacterium glutamicum	100,000	10-Feb-99
		GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	68,003	24-Jun-98
		GB_BA1:MTU88526	2412	U88526	Mycobacterium tuberculosis putative alpha-isopropyl malate synthase (leuA) gene, complete cds.	Mycobacterium tuberculosis	68,185	28-Feb-97

TABLE 4: ALIGNMENT RESULTS

rx00537	2409	GB_BA2:SCD25	41822	AL118514	Streptomyces coelicolor cosmid D25.	Streptomyces coelicolor A3(2)	83,187	21-Sep-99
		GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.	Mycobacterium tuberculosis	62,401	17-Jun-98
		GB_BA1:MTU34956	2462	U34956	Mycobacterium tuberculosis phosphoribosylformylglycinamide synthase (purL) gene, complete cds.	Mycobacterium tuberculosis	62,205	28-Jan-97
rx00541	792	GB_PAT:192052	2115	I92052	Sequence 19 from patent US 5726299.	Unknown.	98,359	01-DEC-1998
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	62,468	24-Jun-97
		GB_BA1:MTCY369	38850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	60,814	17-Jun-98
rx00558	1470	GB_BA1:BAPURF	1885	X91252	B. ammoniagenes purF gene.	Corynebacterium ammoniagenes	66,095	5-Jun-97
		GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2286.	Mycobacterium leprae	64,315	09-MAR-1995
		GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.	Mycobacterium tuberculosis	64,863	17-Jun-98
rx00579	1983	GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	98,810	05-DEC-1998
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	98,810	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	98,810	24-Jun-98
rx00580	1425	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	99,368	24-Jun-98
		GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	99,368	05-DEC-1998
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	99,368	08-OCT-1997 (Rel. 52, Created)
rx00581	1092	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	37,071	24-Jun-98
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	37,071	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	37,071	05-DEC-1998
rx00584	1248	GB_BA1:CORAHP5	2570	L07603	Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene, complete cds.	Corynebacterium glutamicum	98,236	26-Apr-93
		GB_BA1:AOPCZA361	37841	AJ223998	Amycolatopsis orientalis cosmid PCZA361.	Amycolatopsis orientalis	54,553	29-MAR-1999
		GB_BA1:D90714	14358	D90714	Escherichia coli genomic DNA. (16.8 - 17.1 min).	Escherichia coli	53,312	7-Feb-99
rx00618	1230	GB_EST19:AA602737	260	AA602737	GM06238.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM06238 5prime, mRNA sequence.	Drosophila melanogaster	39,928	25-Nov-98
		GB_EST28:A1534381	581	A1534381	SD07186.5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD07186 5prime similar to X89858: Ant FBgn0011558 PID:g927407 SPTREMBL:Q24240, mRNA sequence.	Drosophila melanogaster	41,138	18-MAR-1999
		GB_IN1:DMANILLIN	4029	X89858	D. melanogaster mRNA for anillin protein.	Drosophila melanogaster	34,398	6-Nov-95
rx00619	1551	GB_BA1:MTCY369	38850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 38/162.	Mycobacterium tuberculosis	62,778	17-Jun-98
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	61,831	24-Jun-97
		GB_PAT:A60305	1845	A60305	Sequence 5 from Patent WO9708323.	unidentified	61,785	06-MAR-1998
rx00620	1014	GB_PL2:AF063247	1450	AF063247	Pneumocystis carinii f. sp. ratt encodes mRNA, complete cds.	Pneumocystis carinii f. sp. rattii	41,060	5-Jan-99
		GB_BA1:STNAPP	2069	M91546	Streptomyces lividans aminopeptidase P (PepP) gene, complete cds.	Streptomyces lividans	37,126	12-Jun-93

TABLE 4: ALIGNMENT RESULTS

GB_HTG3:AC008783	214575	AC008783	Homo sapiens chromosome 19 clone CITB-E1_3214H19, *** SEQUENCING IN PROGRESS ***, 21 unordered pieces.	Homo sapiens	40,020	3-Aug-99
GB_IN1:CEY41E3	150541	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence	Caenorhabditis elegans	36,986	2-Sep-99
GB_EST13:AA392187	372	AA362187	EST1561 Macrophage 1 Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	38,378	21-Apr-97
GB_IN1:CEY41E3	150541	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	37,694	2-Sep-99
GB_BA1:MTCY309	36850	Z60226	Mycobacterium tuberculosis H37Rv complete genome; segment 38/182.	Mycobacterium tuberculosis	57,971	17-Jun-98
GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	58,808	24-Jun-97
GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L288.	Mycobacterium leprae	38,007	09-MAR-1995
GB_BA1:BRLBIOD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and delhiobiotin synthetase, complete cds.	Corynebacterium glutamicum	97,358	3-Feb-99
GB_PAT:E04041	675	E04041	DNA sequence coding for deshiobiotin synthetase.	Corynebacterium glutamicum	98,074	29-Sep-97
GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	93,814	29-Sep-97
GB_BA1:BRLBIOD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and delhiobiotin synthetase, complete cds.	Corynebacterium glutamicum	95,690	3-Feb-99
GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	95,755	29-Sep-97
GB_BA2:EHU38519	1290	U38519	Erwinia herbicola adenosylmethionine-8-amino-7-oxononanoate transaminase (bioA) gene, complete cds.	Erwinia herbicola	55,564	4-Nov-98
GB_BA1:MTV041	28826	AL021958	Mycobacterium tuberculosis H37Rv complete genome; segment 35/162.	Mycobacterium tuberculosis	60,030	17-Jun-98
GB_BA1:BRLSECY	1516	D14162	Brevibacterium flavum gene for SecY protein (complete cds) and gene or adenylate Kinase (partial cds).	Corynebacterium glutamicum	99,583	3-Feb-99
GB_BA2:MBU77912	7163	U77912	Mycobacterium bovis MBE50a gene, partial cds; and MBE50b, MBE50c, preprotein translocase SecY subunit (secY), adenylate kinase (adk), methionine aminopeptidase (map), RNA polymerase ECF sigma factor (sigE50), MBE50d, and MBE50e genes, complete cds.	Mycobacterium bovis	60,030	27-Jan-99
GB_BA2:AF157493	25454	AF157493	Zymomonas mobilis ZM4 fosmid clone 42D7, complete sequence.	Zymomonas mobilis	39,116	5-Jul-99
GB_PAT:I00836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	47,419	21-MAY-1993
GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	47,419	29-Sep-97
GB_PAT:I78753	1187	I78753	Sequence 9 from patent US 5693781.	Unknown.	37,814	3-Apr-98
GB_PAT:I92042	1187	I92042	Sequence 9 from patent US 5726299.	Unknown.	37,814	01-DEC-1998
GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	50,647	17-Jun-98
GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	56,228	17-Jun-98
GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	40,300	17-Jun-98
GB_GSS12:AQ420755	671	AQ420755	RPC1-11-188G18.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-188G18, genomic survey sequence.	Homo sapiens	35,750	23-MAR-1999
GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPC1-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces.	Drosophila melanogaster	40,634	6-Aug-99
GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPC1-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces.	Drosophila melanogaster	40,634	6-Aug-99
GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPC1-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces.	Drosophila melanogaster	33,888	6-Aug-99

TABLE 4: ALIGNMENT RESULTS

rx00766	966	GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***; 2 Caenorhabditis elegans unordered pieces.	36,737	25-Feb-99
		GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***; 2 Caenorhabditis elegans unordered pieces.	36,737	25-Feb-99
rx00770	1293	GB_BA1:D00810	20476	D00810	E.coli genomic DNA, Kohara clone #318(37.4-37.8 min.).	36,526	29-MAY-1997
		GB_BA1:MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	66,193	24-Jun-99
		GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	61,443	09-MAR-1995
		GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	59,938	21-Sep-99
rx00779	1056	GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	64,896	14-OCT-1998
		GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	64,896	14-OCT-1998
		GB_PL2:AF078693	1492	AF078693	Chlamydomonas reinhardtii putative O-acetylserine(thiol)lyase precursor (Crys-1A) mRNA, nuclear gene encoding organellar protein, complete cds.	57,970	3-Nov-99
rx00780	669	GB_BA1:MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	54,410	17-Jun-98
		GB_BA1:AVINIFREG	7099	M60090	Azotobacter chroococcum nifU, nifS, nifV, nifP, nifW, nifZ and nifM genes, complete cds.	51,729	26-Apr-93
		GB_BA2:AF001780	6701	AF001780	Cyanobacterium PCC 8801 NifP (nifP), nitrogenase (nifB), FdxN (fdxN), NifS (nifS) and NifU (nifU) genes, complete cds, and NifH (nifH) gene, partial cds.	36,309	08-MAR-1999
rx00838	1023	GB_EST1:Z30506	329	Z30506	ATTS2430 AC16H Arabidopsis thaliana cDNA clone TAI308 3', mRNA sequence.	44,308	11-MAR-1994
		GB_PL2:AC006258	110469	AC006258	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence.	35,571	28-DEC-1998
		GB_EST37:A1998439	455	A1998439	701545695 A. thaliana, Columbia Col-0, rosette-2 Arabidopsis thaliana cDNA clone 701545695, mRNA sequence.	36,044	8-Sep-99
rx00863	867	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	99,539	16-Aug-93
		GB_PAT:E16749	2001	E16749	gDNA encoding dihydrodipicolinate synthase (DDPS).	99,539	28-Jul-99
		GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinate acid synthase.	99,539	28-Jul-99
rx00864	873	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	98,885	16-Aug-93
		GB_BA1:CGDAPB	1902	X67737	C.glutamicum dapB gene for dihydrodipicolinate reductase.	100,000	1-Apr-93
		GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinate acid synthase.	100,000	28-Jul-99
rx00865	1026	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	100,000	16-Aug-93
		GB_PAT:E16752	1411	E16752	gDNA encoding dihydrodipicolinate reductase (DDPR).	99,805	28-Jul-99
		GB_PAT:AR038113	1411	AR038113	Sequence 18 from patent US 5804414.	98,805	28-Sep-99
rx00867	650	GB_BA1:MTV002	58414	AL008867	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	39,179	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	39,482	22-Aug-97
		GB_BA1:SAU19858	2838	U19858	Streptomyces antibioticus guanosine pentaphosphate synthetase (gpsl) gene, complete cds.	68,708	25-OCT-1996
rx00873	779	GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	63,415	29-MAR-1999
		GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism cluster I.	61,617	29-MAR-1999

TABLE 4: ALIGNMENT RESULTS

rx000884	1263	GB_BA1:D78198 GB_BA1:MTCY253 GB_BA1:MSGY222 GB_GSS15:AQ654600	2304 41230 41156 468	D78198 Z81368 AD000010 AQ654600	Pimelobacter sp. DNA for trehalase synthase, complete cds. Mycobacterium tuberculosis H37Rv complete genome; segment 108/162. Mycobacterium tuberculosis sequence from clone y222. Sheared DNA-1014. TF Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-1014, genomic survey sequence.	60,594 37,785 38,006 33,974	Pimelobacter sp. Mycobacterium tuberculosis Mycobacterium tuberculosis Trypanosoma brucei	5-Feb-99 17-Jun-98 03-DEC-1996 22-Jun-99
rx000891	1102	GB_BA1:MTCI418B GB_BA1:SCO001206 GB_BA1:SCO001205 EM_PAT:E10963	11700 9184 9589 3118	Z96071 AJ001206 AJ001205 E10963	Mycobacterium tuberculosis H37Rv complete genome; segment 7/162. Streptomyces coelicolor A3(2), glycogen metabolism cluster II. Streptomyces coelicolor A3(2) glycogen metabolism cluster. gDNA encoding tryptophan synthase.	63,297 61,965 61,727 99,688	Mycobacterium tuberculosis Streptomyces coelicolor Streptomyces coelicolor Corynebacterium glutamicum	18-Jun-98 29-MAR-1999 29-MAR-1999 08-OCT-1997 (Rel. 52, Created)
rx000954	644	GB_BA1:BLTRP GB_PAT:E01688 GB_PAT:E01375 GB_PAT:E01688 GB_BA1:BLTRP GB_PAT:E01375 GB_BA1:BLTRP GB_PAT:E01688 GB_PAT:E01688 EM_PAT:E10963	7725 7725 7726 7725 7725 7726 7725 7725 7725 3118	X04960 E01688 E01375 E01688 X04960 E01375 X04960 E01688 E01688 E10963	Brevibacterium lactofermentum tryptophan operon. Genomic DNA of trp operon of prepriobacterium latopheimentamn. DNA sequence of tryptophan operon. Genomic DNA of trp operon of prepriobacterium latopheimentamn. Brevibacterium lactofermentum tryptophan operon. DNA sequence of tryptophan operon. Brevibacterium lactofermentum tryptophan operon. Genomic DNA of trp operon of prepriobacterium latopheimentamn. gDNA encoding tryptophan synthase.	98,847 98,428 98,758 98,758 98,758 98,372 98,372 98,242 98,949	Corynebacterium glutamicum unidentified Corynebacterium glutamicum unidentified Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum unidentified Corynebacterium glutamicum	10-Feb-99 29-Sep-97 29-Sep-97 29-Sep-97 10-Feb-99 29-Sep-97 10-Feb-99 29-Sep-97 08-OCT-1997 (Rel. 52, Created)
rx000957	1677	GB_BA1:BLTRP GB_PAT:E01375 GB_BA1:BLTRP GB_PAT:E01375 GB_PAT:E01688 GB_BA1:BLTRP GB_PAT:E01375 GB_PAT:E01688 GB_BA1:CGHOMTHR	7725 7726 7725 7726 7725 7725 7726 7725 3685	X04960 E01375 X04960 E01375 E01688 X04960 E01375 E01688 Y00546	Brevibacterium lactofermentum tryptophan operon. DNA sequence of tryptophan operon. Brevibacterium lactofermentum tryptophan operon. DNA sequence of tryptophan operon. Genomic DNA of trp operon of prepriobacterium latopheimentamn. Brevibacterium lactofermentum tryptophan operon. DNA sequence of tryptophan operon. Genomic DNA of trp operon of prepriobacterium latopheimentamn. Corynebacterium glutamicum hom-lhrB genes for homoserine dehydrogenase and homoserine kinase.	99,107 98,945 99,165 98,927 98,867 98,782 98,782 98,658 98,905	Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum unidentified Corynebacterium glutamicum Corynebacterium glutamicum unidentified Corynebacterium glutamicum	10-Feb-99 29-Sep-97 10-Feb-99 29-Sep-97 29-Sep-97 10-Feb-99 29-Sep-97 29-Sep-97 12-Sep-93
rx000972	1458	GB_PAT:109077 GB_PAT:E01358 GB_PAT:E16755	3685 2615 3579	I09077 E01358 E16755	Sequence 1 from Patent WO 8809819. DNA encoding for homoserine dehydrogenase(HDH)and homoserine kinase(HK). gDNA encoding diaminopimelate decarboxylase (DDC) and arginyl-IRNA synthase.	99,810 97,524 99,931	Unknown. Corynebacterium glutamicum Corynebacterium glutamicum	02-DEC-1994 29-Sep-97 28-Jul-99
rx000981	753	GB_PAT:AR038110 GB_PAT:E14508 GB_OV:GGA245884 GB_PL2:AC007887	3579 3579 512 159434	AR038110 E14508 AJ245884 AC007887	Sequence 15 from patent US 5804414. DNA encoding Brevibacterium diaminopimelic acid decarboxylase and arginyl-IRNA synthase. Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene). Genomic sequence for Arabidopsis thaliana BAC F1504 from chromosome 1, complete sequence.	98,831 99,931 37,538 37,600	Unknown. Corynebacterium glutamicum Gallus gallus Arabidopsis thaliana	29-Sep-99 28-Jul-99 28-Sep-99 04-OCT-1998



TABLE 4: ALIGNMENT RESULTS

	GB_GSS1:CNS00RNW 542	AL087338	Arabidopsis thaliana genome survey sequences T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequences.	Arabidopsis thaliana	41,264	28-Jun-99
rx00989 1644	GB_BA1:MTV008 63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	40,773	17-Jun-98
	GB_BA1:SCVALSFP 3619	Y13070	S.coelicolor valS, fpgs, ndk genes.	Streptomyces coelicolor	58,119	03-MAR-1998
	GB_BA1:MTV008 63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	38,167	17-Jun-98
rx00997 705	GB_BA2:CGU31225 1817	U31225	Corynebacterium glutamicum L-proline:NADP+ 5-oxoreductase (proC) gene, complete cds.	Corynebacterium glutamicum	40,841	2-Aug-98
	GB_HTG1:CEY39C12 282838	AL009028	Caenorhabditis elegans chromosome IV clone Y39C12, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Caenorhabditis elegans	38,416	28-OCT-1999
	GB_IN1:CEB0001 39416	Z69834	Caenorhabditis elegans cosmid B0001, complete sequence.	Caenorhabditis elegans	38,416	2-Sep-99
rx01019 1110	GB_HTG2:AC005052 144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS *** 3 unordered pieces.	Homo sapiens	39,172	12-Jun-98
	GB_HTG2:AC005052 144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS *** 3 unordered pieces.	Homo sapiens	39,172	12-Jun-98
	GB_GSS9:AQ171808 512	AQ171808	HS_3179_A1_G03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens sapiens genomic clone Plate=3179 Col=5 Row=M, genomic survey sequence.	Homo sapiens	34,661	17-OCT-1998
rx01028 1782	GB_BA1:SC1C2 42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	68,275	15-Jan-99
	GB_BA1:ATLEUCD 2982	X84647	A.tetrahymyceticus leuC and leuD genes.	Actinoplanes tetrahymyceticus	65,935	04-OCT-1995
rx01027 1131	GB_BA1:MTV012 70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	40,454	23-Jun-98
	GB_BA1:MLCB637 44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	38,638	17-Sep-97
	GB_BA1:MTCY349 43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	51,989	17-Jun-98
	GB_BA1:SPUNG MUTX 1172	Z21702	S.pneumoniae ung gene and muX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase.	Streptococcus pneumoniae	38,088	15-Jun-94
rx01073 954	GB_BA1:BACOUTB 1004	M15811	Bacillus subtilis outB gene encoding a sporulation protein, complete cds.	Bacillus subtilis	53,723	26-Apr-93
	GB_PR4:AC007938 187237	AC007938	Homo sapiens clone UWGC:djs201 from 7q31, complete sequence.	Homo sapiens	34,322	1-Jul-99
	GB_PL2:ATAC006282 92577	AC006282	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence.	Arabidopsis thaliana	36,181	13-MAR-1999
rx01079 2228	GB_BA2:AF112535 4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	Corynebacterium glutamicum	98,820	5-Aug-89
	GB_BA1:CANRDFGEN 6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	75,968	18-Apr-98
rx01080 567	GB_BA1:MTV012 70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	38,288	23-Jun-99
	GB_BA2:AF112535 4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	Corynebacterium glutamicum	100,000	5-Aug-99
	GB_BA1:CANRDFGEN 6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	65,511	18-Apr-98
rx01087 999	GB_BA1:STNRD 4894	X73226	S.lyophilum nrdE operon.	Salmonella typhimurium	52,477	03-MAR-1997
	GB_IN2:AF063412 1093	AF063412	Llmadia lenticularis elongation factor 1-alpha mRNA, partial cds.	Llmadia lenticularis	43,750	29-MAR-1999
	GB_PR3:HS24M15 134539	Z94055	Human DNA sequence from PAC 24M15 on chromosome 1. Contains tenascin-R (restridin), EST.	Homo sapiens	37,475	23-Nov-99
	GB_IN2:ARU85702 1240	U85702	Anathix ralla, elongation factor-1 alpha (EF-1a) gene, partial cds.	Anathix ralla	37,319	18-Jul-87

TABLE 4: ALIGNMENT RESULTS

rx01095	857	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	43,243	17-Jun-98
		GB_HTG5:AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,471	19-Nov-99
		GB_HTG5:AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,836	19-Nov-99
rx01097	477	GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	100,000	13-Nov-97
		GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	41,206	13-Nov-97
rx01098	897	GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	97,933	13-Nov-97
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	40,972	10-DEC-1998
		GB_BA1:MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	61,366	27-Aug-99
rx01100	861	GB_BA2:AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	97,154	12-MAR-1998
		GB_BA2:AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	95,455	29-Apr-98
		GB_HTG1:HSDJ140A9	221755	AL109917	Homo sapiens chromosome 1 clone RP1-140A9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	30,523	23-Nov-98
rx01101	756	GB_BA2:AF060558	838	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	94,462	29-Apr-98
		GB_BA1:SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	38,378	23-Jul-99
rx01104	729	GB_BA1:STMHISOPA	3981	M31628	S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor	60,053	28-Apr-93
		GB_BA1:STMHISOPA	3981	M31628	S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor	58,333	26-Apr-93
		GB_BA1:SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	39,045	23-Jul-99
rx01105	1221	GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	60,364	24-Jun-99
		GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	60,931	24-Jun-99
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	36,851	10-DEC-1998
		GB_BA1:MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	60,902	27-Aug-99
rx01108	1448	GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	37,233	10-DEC-1998
		GB_BA1:MSHISC	2298	X85542	M.smegmatis genes hisD and hisC for histidinol dehydrogenase and histidinol phosphate aminotransferase, respectively.	Mycobacterium smegmatis	60,111	30-Jun-93
rx01145	1137	GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	58,420	24-Jun-99
		GB_BA1:CORAIA	4705	L09232	Corynebacterium glutamicum acetoaldehyde synthase (livB) and (livN) genes, and acetoaldehyde acid isomerase (livC) gene, complete cds.	Corynebacterium glutamicum	100,000	23-Feb-95
		GB_BA1:BRLLVCA	1364	D14551	Brevibacterium flavum livC gene for acetoaldehyde acid isomerase, complete cds.	Corynebacterium glutamicum	99,580	3-Feb-99
rx01182	1449	GB_PAT:E08232	1017	E08232	DNA encoding acetoaldehyde-add isomerase.	Corynebacterium glutamicum	99,803	28-Sep-97
		GB_PAT:A60299	2869	A60299	Sequence 18 from Patent WO9706261.	Aspergillus niger	38,675	06-MAR-1998
		GB_PR3:HS24E5	35506	Z82185	Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.	Homo sapiens	36,204	23-Nov-99

TABLE 4: ALIGNMENT RESULTS

GB_PR3:AC005265	43900	AC005265	Homo sapiens chromosome 19, cosmid F19750, complete sequence.	Homo sapiens	38,363	6-Jul-98
GB_HTG2:AC004965	323792	AC004965	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,058	12-Jun-98
GB_HTG2:AC004965	323792	AC004965	unordered pieces.			
GB_HTG2:AC004965	323792	AC004965	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,058	12-Jun-98
GB_PL2:TAU55859	2387	U55859	unordered pieces.			
GB_HTG3:AC011469	113436	AC011469	Triticum aestivum heat shock protein 80 mRNA, complete cds.	Triticum aestivum	37,268	1-Feb-99
GB_HTG3:AC011469	113436	AC011469	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***	Homo sapiens	40,000	07-OCT-1999
GB_HTG3:AC011469	113436	AC011469	31 unordered pieces.			
GB_PL1:AB010077	77380	AB010077	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***	Homo sapiens	40,000	07-OCT-1999
GB_PL1:AB010077	77380	AB010077	31 unordered pieces.			
GB_BA1:MTCY10G2	38970	Z92539	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence.	Arabidopsis thaliana	36,803	20-Nov-99
GB_IN1:LEIPRP	1887	M70553	Mycobacterium tuberculosis H37Rv complete genome, segment 47/162.	Mycobacterium tuberculosis	37,047	17-Jun-98
GB_HTG2:HSJ799D16	130149	AL050344	Leishmania donovani phosphotyrosyl phosphatase gene, complete cds.	Leishmania donovani	50,738	7-Jun-93
GB_BA1:MTCY48	35377	Z74020	Homo sapiens chromosome 1 clone RP4-799D16 map p34.3-36.1, *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,135	25-Nov-99
GB_PR2:AB028032	6377	AB028032	unordered pieces.			
GB_GSS9:AQ107201	355	AQ107201	Mycobacterium tuberculosis H37Rv complete genome, segment 89/162.	Mycobacterium tuberculosis	38,139	17-Jun-98
GB_PL2:F508	99923	AC005990	Homo sapiens mRNA for KIAA1109 protein, partial cds.	Homo sapiens	39,394	4-Aug-99
GB_PL2:F508	99923	AC005990	HS_3098_A1_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3098 Col=5 Row=E, genomic survey sequence.	Homo sapiens	41,408	28-Aug-98
GB_IN1:CELC06G1	31205	U41014	Arabidopsis thaliana chromosome 1 BAC F508 sequence, complete sequence.	Arabidopsis thaliana	36,118	23-DEC-1998
GB_GSS14:AQ518843	441	AQ518843	Arabidopsis thaliana chromosome 1 BAC F508 sequence, complete sequence.	Arabidopsis thaliana	35,574	23-DEC-1998
GB_HTG2:AC007473	194859	AC007473	Caenorhabditis elegans cosmid C06G1.	Caenorhabditis elegans	38,560	30-Nov-95
GB_HTG4:AC011696	115847	AC011696	HS_5108_A1_D10_SP06 RPCL-11 Human Male BAC Library Homo sapiens genomic clone Plate=882 Col=19 Row=G, genomic survey sequence.	Homo sapiens	41,121	05-MAY-1999
GB_PL2:ATAC005167	83260	AC005167	Drosophila melanogaster chromosome 2 clone BACR38D12 (D590) RPCL-98	Drosophila melanogaster	40,634	2-Aug-99
GB_PL2:ATAC005825	97380	AC005825	38 D.12 map 48A-48B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***			
GB_HTG3:AC011150	127222	AC011150	60 unordered pieces.			
GB_EST32:A1725583	728	A1725583	Drosophila melanogaster chromosome 2 clone BACR35F01 (D1156) RPCL-98	Drosophila melanogaster	38,290	28-OCT-1999
GB_PR2:HS227P17	82951	Z81007	35 F.1 map 48A-48C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***			
GB_PL2:ATAC005167	83260	AC005167	108 unordered pieces.			
GB_PL2:ATAC005825	97380	AC005825	Arabidopsis thaliana chromosome 11 BAC F12A24 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	15-OCT-1998
GB_HTG3:AC011150	127222	AC011150	Arabidopsis thaliana chromosome 11 BAC F12A24 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	12-Apr-99
GB_EST32:A1725583	728	A1725583	Homo sapiens clone 4_K_17, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	37,722	01-OCT-1999
GB_PR2:HS227P17	82951	Z81007	BNLGH12371 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U86081) root hair defective 3 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,492	11-Jun-99
			Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST.	Homo sapiens	39,738	23-Nov-99

TABLE 4: ALIGNMENT RESULTS

GB_EST34:AV171099	173	AV171099	AV171099 Mus musculus head C57BL/6J 14, 17 day embryo Mus musculus cDNA clone 320002M11, mRNA sequence.	Mus musculus	46,237	6-Jul-99
GB_RO:AB008915S1	530	AB008915	Mus musculus mGp1 gene, exon 1.	Mus musculus	45,574	28-Sep-99
GB_EST22:AI050532	293	AI050532	uc83d10.y1 Sugano mouse kidney mKia Mus musculus cDNA clone IMAGE:1432243 5' similar to TR:O35120 O35120 MGPIIP.1, mRNA sequence.	Mus musculus	44,097	9-Jul-98
GB_RO:AB008895	3082	AB008895	Mus musculus mRNA for mGp1p, complete cds.	Mus musculus	41,316	23-Nov-97
GB_PL1:AB005237	87835	AB005237	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence.	Arabidopsis thaliana	38,608	20-Nov-99
GB_GSS5:AQ766840	491	AQ766840	HS_2026_A2_C09_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=18 Row=E, genomic survey sequence.	Homo sapiens	37,916	28-Jul-99
GB_BA1:MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	Mycobacterium tuberculosis	37,419	24-Jun-99
GB_BA1:CGLYSEG	2374	X98471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	34,831	24-Feb-97
GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	35,138	27-Jul-98
GB_PR3:AC004054	112184	AC004054	Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.	Homo sapiens	37,277	9-Jul-98
GB_BA1:CGLYSEG	2374	X98471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	100,000	24-Feb-97
GB_GSS5:AQ769223	500	AQ769223	HS_3155_B2_G10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3155 Col=20 Row=N, genomic survey sequence.	Homo sapiens	38,400	28-Jul-99
GB_BA1:CGLYSEG	2374	X98471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	33,665	24-Feb-97
GB_BA1:SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.	Streptomyces coelicolor	62,726	10-Aug-98
GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	39,159	22-Aug-97
GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,340	17-Jun-98
GB_BA1:D90827	18886	D90827	E.coli genomic DNA, Kohara clone #336(41.2-41.6 min.).	Escherichia coli	58,517	21-MAR-1997
GB_BA1:D90828	14590	D90828	E.coli genomic DNA, Kohara clone #338gap(41.6-41.9 min.).	Escherichia coli	58,151	21-MAR-1997
GB_BA2:AE000279	10855	AE000279	Escherichia coli K-12 MG1655 section 169 of 400 of the complete genome.	Escherichia coli	58,021	12-Nov-98
GB_BA1:SCH10	39524	AL049754	Streptomyces coelicolor cosmid H10.	Streptomyces coelicolor	39,037	04-MAY-1999
GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	40,130	17-Jun-98
GB_BA1:MLCB4	36310	AL023514	Mycobacterium leprae cosmid B4.	Mycobacterium leprae	37,752	27-Aug-99
GB_BA1:MTY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	Mycobacterium tuberculosis	39,057	17-Jun-98
GB_BA1:MSGB1229CS	30670	L78812	Mycobacterium leprae cosmid B1229 DNA sequence.	Mycobacterium leprae	54,382	15-Jun-98
GB_BA2:AF027507	5168	AF027507	Mycobacterium smegmatis dGTPase (dgtl) and primase (dnaG) genes, complete cds; RNA-Asn gene, complete sequence.	Mycobacterium smegmatis	52,941	18-Jan-98
GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	40,941	17-Jun-98
GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	38,451	22-Aug-97
GB_BA1:SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.	Streptomyces coelicolor	61,194	10-Aug-98
GB_BA1:CORFADS	1547	D37967	Corynebacterium ammoniagenes gene for FAD synthetase, complete cds.	Corynebacterium ammoniagenes	58,021	8-Feb-99
GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	38,414	22-Aug-97
GB_BA1:SC10A7	39739	AL078618	Streptomyces coelicolor cosmid 10A7.	Streptomyces coelicolor	38,930	9-Jun-99
GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,062	17-Jun-98

TABLE 4: ALIGNMENT RESULTS

GB_EST13:AA356958	255	AA356958	EST65614 Jurkat T-cells III Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	37,647	21-Apr-97
GB_OV:OMDNAPROI	7327	X92380	O.mossambicus prolactin I gene.	Tilapia mossambica	38,289	19-OCT-1985
GB_IN1:CEF28C12	14653	Z93380	Caenorhabditis elegans cosmid F28C12, complete sequence.	Caenorhabditis elegans	37,984	23-Nov-98
GB_IN1:CEF28C12	14653	Z93380	Caenorhabditis elegans cosmid F28C12, complete sequence.	Caenorhabditis elegans	38,469	23-Nov-98
GB_BA1:SCE9	37730	AL049841	Streptomyces coelicolor cosmid E9.	Streptomyces coelicolor	39,021	19-MAY-1999
GB_BA1:MAU88875	840	U88875	Mycobacterium avium hypoxanthine-guanine phosphoribosyl transferase gene, complete cds.	Mycobacterium avium	57,521	05-MAR-1997
GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	40,086	17-Jun-98
GB_BA1:MTCY7H7B	24244	Z95557	Mycobacterium tuberculosis H37Rv complete genome; segment 153/162.	Mycobacterium tuberculosis	43,343	18-Jun-98
GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	38,177	27-Aug-99
GB_PL1:EGGTPCHI	242	Z49757	E.gracilis mRNA for GTP cyclohydrolase I (core region).	Euglena gracilis	64,876	20-OCT-1995
GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,943	17-Apr-98
GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,500	17-Apr-98
GB_BA1:MTCY49	39430	Z73966	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162.	Mycobacterium tuberculosis	38,010	24-Jun-99
GB_IN1:DME238847	5419	AJ238847	Drosophila melanogaster mRNA for drosophila dodeca-satellite protein 1 (DDP-Drosophila melanogaster 1).	Drosophila melanogaster	36,346	13-Aug-99
GB_HTG3:AC009210	103814	AC009210	Drosophila melanogaster chromosome 2 clone BACR0106 (D1054) RPC1-98 01.1.6 map 55D-55D strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***.	Drosophila melanogaster	37,897	20-Aug-99
GB_IN2:AF132179	4842	AF132179	Drosophila melanogaster clone LD21677 unknown mRNA.	Drosophila melanogaster	36,149	3-Jun-99
GB_PL2:F6H8	82596	AF178045	Arabidopsis thaliana BAC F6H8.	Arabidopsis thaliana	35,846	19-Aug-99
GB_PL2:AF038831	847	AF038831	Sorosporium saporariae internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.	Sorosporium saporariae	40,566	13-Apr-99
GB_PL2:ATAC005957	108355	AC005957	Arabidopsis thaliana chromosome II BAC T15/14 genomic sequence, complete sequence.	Arabidopsis thaliana	38,095	7-Jan-99
GB_BA1:ANANIFBH	5936	J05111	Anabaena sp. (clone AnH20.1) nitrogen fixation operon nifB, fdxN, nifS, nifU, and nifH genes, complete cds.	Anabaena sp.	38,206	26-Apr-93
GB_PR2:AC002461	197273	AC002461	Human BAC clone RG204116 from 7q31, complete sequence.	Homo sapiens	38,623	20-Aug-97
GB_PR2:AC002461	197273	AC002461	Human BAC clone RG204116 from 7q31, complete sequence.	Homo sapiens	34,719	20-Aug-97
GB_RO:MM437P9	165901	AL049866	Mus musculus chromosome X, clone 437P9.	Mus musculus	37,500	29-Jun-99
GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	37,031	01-OCT-1998
GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	38,035	01-OCT-1998
GB_BA1:MTCY22G10	35420	Z84724	Mycobacterium tuberculosis H37Rv complete genome; segment 21/162.	Mycobacterium tuberculosis	38,371	17-Jun-98
GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	38,064	17-DEC-1993
GB_BA1:SCQ11	15441	AL096823	Streptomyces coelicolor cosmid Q11.	Streptomyces coelicolor	60,776	8-Jul-99
GB_IN4:HSU51003	47396	AL032630	Caenorhabditis elegans cosmid Y62H9A, complete sequence.	Caenorhabditis elegans	38,514	2-Sep-99
GB_PR4:HSU51003	3202	U51003	Homo sapiens DLX-2 (DLX-2) gene, complete cds.	Homo sapiens	37,730	07-DEC-1998
GB_OM:PIGDAO1	395	M18444	Pig D-amino acid oxidase (DAO) gene, exon 1.	Sus scrofa	39,340	27-Apr-83
GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	63,300	17-Jun-98
GB_BA1:U00021	39193	U00021	Mycobacterium leprae cosmid L247.	Mycobacterium leprae	36,756	28-Sep-94
GB_BA1:MLCB1351	38936	Z95117	Mycobacterium leprae cosmid B1351.	Mycobacterium leprae	36,756	24-Jun-97

TABLE 4: ALIGNMENT RESULTS

rx01617	795	GB_PR2:HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657.	Homo sapiens	40,811	5-Jul-99
		GB_PR2:HS13D10	153147	AL021407	Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.	Homo sapiens	38,788	23-Nov-99
rx01657	723	GB_PR2:HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657.	Homo sapiens	39,018	5-Jul-99
		GB_BA1:MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome; segment 117/162.	Mycobacterium tuberculosis	40,666	17-Jun-98
		GB_EST8:D79278	392	D79278	HUM213D068 Human aorta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-213D06 5', mRNA sequence.	Homo sapiens	44,262	9-Feb-98
rx01660	875	GB_BA2:AF129925	10243	AF129925	Thiobacillus ferrooxidans carboxysome operon, complete cds.	Thiobacillus ferrooxidans	40,709	17-MAY-1999
		GB_BA1:MTV013	11364	AL021309	Mycobacterium tuberculosis H37Rv complete genome; segment 134/162.	Mycobacterium tuberculosis	40,986	17-Jun-98
		GB_RO1:MFV1	6480	X97719	M. musculus reitovirus restriction gene Fv1.	Mus musculus	35,364	28-Aug-96
		GB_PAT:A67508	6480	A67508	Sequence 1 from Patent WO9743410.	Mus musculus	35,364	05-MAY-1998
rx01678	651	GB_VI:TVU95309	600	U95309	Tula virus O64 nucleocapsid protein gene partial cds.	Tula virus	41,894	28-OCT-1997
		GB_VI:TVU95303	600	U95303	Tula virus O52 nucleocapsid protein gene partial cds.	Tula virus	41,712	28-OCT-1997
		GB_VI:TVU95302	600	U95302	Tula virus O24 nucleocapsid protein gene partial cds.	Tula virus	39,576	28-OCT-1997
rx01679	1359	GB_EST5:H81843	362	H91843	ya01601.81 Soares retina NZB4HR Homo sapiens cDNA clone IMAGE:221208 3' similar to gb:X63749_ma1 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-1 (HUMAN); mRNA sequence.	Homo sapiens	39,157	29-Nov-95
rx01690	1224	GB_STS:G26925	362	G26925	human STS SHGC-30023, sequence tagged site.	Homo sapiens	39,157	14-Jun-96
		GB_PL2:AF139451	1202	AF139451	Gossypium robinsonii CeiA2 pseudogene, partial sequence.	Gossypium robinsonii	38,910	1-Jun-99
		GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	60,644	15-Jan-99
		GB_EST22:A1064232	493	A1064232	GH04563.5 prime GH Drosophila melanogaster head POT2 Drosophila melanogaster cDNA clone GH04563 5 prime, mRNA sequence.	Drosophila melanogaster	38,037	24-Nov-98
rx01692	873	GB_IN2:AF117896	1020	AF117896	Drosophila melanogaster neuropeptide F (npr) gene, complete cds.	Drosophila melanogaster	36,122	2-Jul-99
		GB_BA2:AF087123	1034	AF087123	Lactobacillus reuteri cobalamin biosynthesis protein J (cblJ) gene, partial cds; and uroporphyrin-III C-methyltransferase (sumT) gene, complete cds.	Lactobacillus reuteri	48,079	3-Jun-98
		GB_RO:RATNFHPEP	3085	M37227	Rat heavy neurofilament (NF-H) polypeptide, partial cds.	Rattus norvegicus	37,083	27-Apr-93
		GB_RO:RSNFH	3085	X13804	Rat mRNA for heavy neurofilament polypeptide NF-H C-terminus.	Rattus sp.	37,093	14-Jul-95
rx01698	1353	GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (eroK), and 3-dehydroquinate synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Corynebacterium glutamicum	100,000	04-MAY-1999
rx01699	693	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	38,323	17-Jun-98
		GB_BA1:MSG8937CS	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	62,780	15-Jun-96
		GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinate synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Corynebacterium glutamicum	100,000	04-MAY-1999
rx01712	805	GB_BA2:AF016585	41097	AF016585	Streptomyces caelestis cytochrome P-450 hydroxylase homolog (nld) gene, partial cds; polyketide synthase modules 1 through 7 (nldA) genes, complete cds; and N-methyltransferase homolog gene, partial cds.	Streptomyces caelestis	40,260	07-DEC-1997
		GB_EST9:C19712	399	C19712	C19712 Rice particle at ripening stage Oryza sativa cDNA clone E10821_1A, mRNA sequence.	Oryza sativa	45,425	24-OCT-1998
		GB_EST21:AA952468	278	AA952468	TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence.	Trypanosoma cruzi	40,876	28-OCT-1998

TABLE 4: ALIGNMENT RESULTS

GB_EST21-AA952466	278	AA952466	TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence.	41,387	29-OCT-1988
GB_HTG1:HSDJ534K7	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces	35,651	23-Nov-99
GB_HTG1:HSDJ534K7	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	35,651	23-Nov-99
GB_EST27:AI447108	431	AI447108	mq91e08 x1 Stralagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:586118 3', mRNA sequence.	39,671	09-MAR-1999
GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from Tq11.23-q21.1, complete sequence.	35,817	18-MAR-1999
GB_PL2:TM018A10	106184	AF013294	Arabidopsis thaliana BAC TM018A10.	35,698	12-Jul-97
GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from Tq11.23-q21.1, complete sequence.	37,243	18-MAR-1999
GB_EST3:R46227	443	R46227	yg52a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.	42,812	22-MAY-1995
GB_EST3:R46227	443	R46227	yg52a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.	42,655	22-MAY-1995
GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	59,294	17-Jun-98
GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	57,584	22-Aug-97
GB_BA1:SC5F7	40024	AL096872	Streptomyces coelicolor cosmid 5F7.	61,810	22-Jul-99
GB_EST21-AA918454	416	AA918454	om38c02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543298 3' similar to WP:F28F8.3 CE09757 SMALL NUCLEAR RIBONUCLEOPROTEIN E., mRNA sequence.	39,655	23-Jun-98
GB_EST4:H34042	345	H34042	EST110563 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone RPNB181 5' end, mRNA sequence.	35,942	2-Apr-98
GB_EST20-AA899038	450	AA899038	NCP6G8T7 Perithecium Neurospora crassa cDNA clone NP6G8 3' end, mRNA sequence.	40,000	12-Apr-98
GB_BA1:AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 6/7.	40,067	22-Jun-99
GB_HTG4:AC010694	115857	AC010694	Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	35,450	16-OCT-1999
GB_HTG4:AC010694	115857	AC010694	Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	35,450	16-OCT-1999
GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, aml gene, ocd gene and 5' sox4 gene.	100,000	7-Jan-99
GB_RO:RATALGL	7601	M24108	Rattus norvegicus (clone A2U42) alpha2u globulin gene, exons 1-7.	38,692	15-DEC-1994
GB_OV:APIGY2	1381	X78272	Anas platyrhynchos (Super M) IgY epsilon heavy chain gene, exon 2.	38,962	15-Feb-99
GB_EST30:AI629479	353	AI629479	486101D10.x1 486 -leal primordia cDNA library from Hake lab Zea mays cDNA, mRNA sequence.	38,109	26-Apr-99
GB_STS:G48245	515	G48245	SHGC-62915 Human Homo sapiens STS genomic, sequence tagged site.	37,021	26-MAR-1999
GB_GSS3:849052	515	B49052	RPC111-4112.TV RPC1-11 Homo sapiens genomic clone RPC1-11-4112, genomic survey sequence.	37,021	8-Apr-99

TABLE 4: ALIGNMENT RESULTS

rx01850	1470	GB_BA2:ECUJW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 87.4 to 76.0 minutes.	Escherichia coli	37,188	U18997
		GB_BA2:AE000392	10345	AE000392	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome.	Escherichia coli	38,021	12-Nov-98
		GB_BA2:U32715	13136	U32715	Haemophilus influenzae Rd section 30 of 163 of the complete genome.	Haemophilus influenzae Rd	39,860	29-MAY-1998
rx01878	1002	GB_HTG1:CEY64F11	177748	Z99778	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,578	14-OCT-1998
rx01892	852	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	35,910	19-Jun-98
		GB_BA1:MLCB250	40603	Z97369	Mycobacterium leprae cosmid B250.	Mycobacterium leprae	64,260	27-Aug-99
		GB_BA1:MSGB1529CS	36985	L78824	Mycobacterium leprae cosmid B1529 DNA sequences.	Mycobacterium leprae	64,260	15-Jun-98
rx01894	878	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,229	19-Jun-98
		GB_IN1:CELF48H5	38886	U41543	Caenorhabditis elegans cosmid F46H5.	Caenorhabditis elegans	38,525	29-Nov-98
		GB_HTG3:AC009204	115633	AC009204	Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPCI-98 03.E.19 map 36E-37C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 94 unordered pieces.	Drosophila melanogaster	31,578	18-Aug-99
rx01920	1125	GB_BA2:AF112538	1798	AF112538	Corynebacterium glutamicum ribonucleotide reductase beta-chain (nrdF) gene, complete cds.	Corynebacterium glutamicum	99,733	5-Aug-99
		GB_BA1:CANRDFGEN	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	70,321	18-Apr-98
		GB_BA2:AF050168	1228	AF050168	Corynebacterium ammoniagenes ribonucleoside diphosphate reductase small subunit (nrdF) gene, complete cds.	Corynebacterium ammoniagenes	72,082	23-Apr-98
rx01928	860	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	100,000	11-MAY-1999
		GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	35,917	15-Sep-99
		GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	33,925	15-Sep-99
rx01929	836	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	100,000	11-MAY-1999
		GB_BA1:XCU33548	8429	U33548	Xanthomonas campestris hrpB pathogenicity locus proteins HrpB1, HrpB2, HrpB3, HrpB4, HrpB5, HrpB6, HrpB7, HrpB8, HrpA1, and ORF62 genes, complete cds.	Xanthomonas campestris pv. vesicatoria	38,749	19-Sep-98
rx01940	1059	GB_BA1:XANHRP86A	1329	M99174	Xanthomonas campestris hrpB6 gene, complete cds.	Xanthomonas campestris	39,305	14-Sep-93
		GB_IN2:CFU43371	1060	U43371	Crithidia fasciculata inosine-uridine preferring nucleoside hydrolase (IUNH) gene, complete cds.	Crithidia fasciculata	61,417	18-Jun-98
		GB_BA2:AE001467	11601	AE001467	Helicobacter pylori, strain J99 section 28 of 132 of the complete genome.	Helicobacter pylori J99	38,660	20-Jan-99
		GB_RO:AF175967	3492	AF175967	Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.	Mus musculus	40,275	28-Sep-99
rx02022	1230	GB_BA1:CGDAPE	1986	X81379	C.glutamicum dapE gene and orf2.	Corynebacterium glutamicum	100,000	8-Aug-95
		GB_BA1:CGDNAAROP	2812	X85985	C.glutamicum ORF3 and aroP gene.	Corynebacterium glutamicum	38,889	30-Nov-97
		GB_BA1:APU47055	6469	U47055	Anabaena PCC7120 nitrogen fixation proteins (nifE, nifN, nifX, nifW) genes, complete cds, and nitrogenase (nifK) and hnsA genes, partial cds.	Anabaena PCC7120	38,647	17-Feb-96
rx02024	859	GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	59,415	17-Jun-98



TABLE 4: ALIGNMENT RESULTS

rx02027	GB_BA1:MSGB1812CS 38503	L01536	M. leprae genomic dna sequence, cosmid b1912.	Mycobacterium leprae	57,093	14-Jun-96
	GB_BA1:MLU15180 38675	U15180	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	57,210	09-MAR-1995
rx02031	GB_BA1:CGGDHA 2037	X72855	C. glutamicum GDHA gene.	Corynebacterium glutamicum	99,317	24-MAY-1993
	GB_BA1:CGGDH 2037	X59404	Corynebacterium glutamicum, gdh gene for glutamate dehydrogenase.	Corynebacterium glutamicum	94,387	30-Jul-99
rx02085	GB_BA1:PAE18494 1628	Y18494	Pseudomonas aeruginosa gdhA gene, strain PAC1.	Pseudomonas aeruginosa	62,247	6-Feb-99
	GB_BA1:MTCY22G8 22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	38,442	17-Jun-98
rx02093	GB_BA1:MLCB33 42224	Z94723	Mycobacterium leprae cosmid B33.	Mycobacterium leprae	58,486	24-Jun-97
	GB_BA1:ECOUW85 91414	M87049	E. coli genomic sequence of the region from 84.5 to 86.5 minutes.	Escherichia coli	52,127	29-MAY-1995
rx02093	GB_EST14:AA448146 452	AA448146	zw82h01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782737 5'.	Homo sapiens	34,163	4-Jun-97
	GB_EST17:AA641937 444	AA641937	mRNA sequence.		35,586	27-OCT-1997
rx02108	GB_PR3:AC003074 143029	AC003074	ns18b10.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1183963 5'.	Homo sapiens	31,917	6-Nov-97
	GB_BA1:SC1A6 37620	AL023498	mRNA sequence.		35,818	13-Jan-99
rx02111	GB_PR4:AC005553 179651	AC005553	Human PAC clone DJ0596009 from 7p15, complete sequence.	Sireptomycetes coelicolor	34,274	31-DEC-1998
	GB_EST3:R49746 397	R49746	Sireptomycetes coelicolor cosmid 1A8.	Homo sapiens	41,162	18-MAY-1995
rx02112	GB_BA1:SC6G10 36734	AL049497	Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.			
	GB_BA1:U00010 41171	U00010	yg71g10.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:38768 5' similar to gb:V00567 BETA-2-MICROGLOBULIN	Sireptomycetes coelicolor	50,791	24-MAR-1999
rx02134	GB_BA1:MTCY338 32437	Z95586	PRECUSOR (HUMAN);, mRNA sequence.	Mycobacterium leprae	37,563	01-MAR-1994
	GB_HTG3:AC010579 157658	AC010579	Sireptomycetes coelicolor cosmid 6G10.	Mycobacterium tuberculosis	39,504	24-Jun-99
rx02134	GB_GSS3:B09839 1191	B09839	Mycobacterium leprae cosmid B1170.	Drosophila melanogaster	37,909	24-Sep-99
	GB_HTG3:AC010579 157658	AC010579	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Arabisopsis thaliana	37,843	14-MAY-1987
rx02134	GB_BA1:SCSECYDNA 6154	X83011	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPL-98	Drosophila melanogaster	37,909	24-Sep-88
	GB_EST32:A1731596 568	A1731596	09.D.8 map 96F-96F strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***.	Sireptomycetes coelicolor	38,533	02-MAR-1998
rx02134	GB_BA1:SCSECYDNA 6154	X83011	121 unordered pieces.	Gossypium hirsutum	33,451	11-Jun-99
	GB_EST32:A1731596 568	A1731596	Sireptomycetes coelicolor secY locus DNA.	Sireptomycetes coelicolor	38,756	02-MAR-1998
rx02134	GB_BA1:SCSECYDNA 6154	X83011	121 unordered pieces.	Gossypium hirsutum	33,451	11-Jun-99
	GB_EST32:A1731596 568	A1731596	Sireptomycetes coelicolor secY locus DNA.	Sireptomycetes coelicolor	38,756	02-MAR-1998

TABLE 4: ALIGNMENT RESULTS

rx02135	1197	GB_PR3:HS525L6	168111	AL023807	Human DNA sequence from clone RP3-525L6 on chromosome 6p22.3-23 Contains CA repeat, STSs, GSSs and a CpG island, complete sequence.	Homo sapiens	34,365	23-Nov-99
		GB_PL2:ATF21P8	85785	AL022347	Arabidopsis thaliana DNA chromosome 4, BAC clone F21P8 (ESSA project).	Arabidopsis thaliana	34,325	9-Jun-99
rx02136	645	GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7123, complete sequence.	Arabidopsis thaliana	33,874	26-Jun-98
		GB_PL2:ATAC005819	57752	AC005819	Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence.	Arabidopsis thaliana	34,123	3-Nov-98
		GB_PL2:F15K9	71097	AC005278	Arabidopsis thaliana chromosome I BAC F15K9 sequence, complete sequence.	Arabidopsis thaliana	31,260	7-Nov-98
rx02139	1862	GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7123, complete sequence.	Arabidopsis thaliana	34,281	28-Jun-98
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	62,904	17-Jun-98
		GB_BA1:MSG81554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-98
		GB_BA1:MSG81551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-98
rx02153	903	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamate phosphatase reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,104	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	99,224	2-Jul-97
		GB_BA1:CGARGCJBD	4355	X86157	C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-88
rx02154	414	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamate phosphatase reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	98,551	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	98,477	2-Jul-97
		GB_BA1:CGARGCJBD	4355	X86157	C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-88
rx02155	1287	GB_BA1:CGARGCJBD	4355	X86157	C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,767	25-Jul-88
		GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamate phosphatase reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,378	1-Jul-98
		GB_BA1:MSG81133CS	42106	L78811	Mycobacterium leprae cosmid B1133 DNA sequence.	Mycobacterium leprae	55,504	15-Jun-88

TABLE 4: ALIGNMENT RESULTS

rx02156	1074	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	1-Jul-98
		GB_BA1:CGARGC:JBD	4355	X86157		Corynebacterium glutamicum	100,000	25-Jul-96
		GB_BA2:AE001816	10007	AE001816	Thermotoga maritima section 128 of 136 of the complete genome.	Thermotoga maritima	50,238	2-Jun-99
rx02157	1296	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,612	1-Jul-98
		GB_BA1:CGARGC:JBD	4355	X86157		Corynebacterium glutamicum	99,612	25-Jul-96
		GB_BA1:MTCY08H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome: segment 73/162.	Mycobacterium tuberculosis	57,278	17-Jun-98
rx02158	1080	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.	Corynebacterium glutamicum	100,000	1-Jul-98
		GB_BA2:AF031518	2045	AF031518		Corynebacterium glutamicum	99,898	5-Jan-99
		GB_BA1:CGARGC:JBD	4355	X86157		Corynebacterium glutamicum	100,000	25-Jul-96
rx02159	636	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.	Corynebacterium glutamicum	99,843	1-Jul-98
		GB_BA2:AF031518	2045	AF031518		Corynebacterium glutamicum	88,679	5-Jan-99
		GB_BA2:AF041436	516	AF041436	Corynebacterium glutamicum arginine repressor (argR) gene, complete cds.	Corynebacterium glutamicum	100,000	5-Jan-99
rx02160	1326	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. Corynebacterium glutamicum argininosuccinate synthetase (argG) gene, complete cds.	Corynebacterium glutamicum	98,774	1-Jul-98
		GB_BA2:AF030520	1206	AF030520		Corynebacterium glutamicum	99,834	19-Nov-97
		GB_BA1:SCARGGH	1909	Z49111	S.clavuligerus argG gene and argH gene (partial).	Streptomyces clavuligerus	65,913	22-Apr-96

TABLE 4: ALIGNMENT RESULTS

rx02162	1554	GB_BA2:AF049897	9198	AF049897	Corynebacterium glutamicum N-acetylglutamate kinase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	88,524	1-Jul-98
		GB_BA2:AF048764	1437	AF048764	Corynebacterium glutamicum argininosuccinate lyase (argH) gene, complete cds.	Corynebacterium glutamicum	87,561	1-Jul-98
rx02176	1251	GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome; segment 73/162.	Mycobacterium tuberculosis	64,732	17-Jun-98
		GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	36,998	17-Jun-98
		GB_BA1:CGGLTG	3013	X68112	C-glutamicum gll gene for citrate synthase and ORF.	Corynebacterium glutamicum	39,910	17-Feb-95
rx02189	861	GB_PL2:PGU65398	2700	U65399	Basidiomycete CECT 20197 phenoloxidase (pox1) gene, complete cds.	basidiomycete CECT 20197	38,474	19-Jul-97
		GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	35,941	16-Sep-98
		GB_BA1:MSG81970CS	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	40,286	15-Jun-98
rx02193	1701	GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	33,689	16-Sep-98
		GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	99,353	6-Feb-99
		GB_PAT:E04307	1581	E04307	DNA encoding Brevibacterium flavum aspartase.	Corynebacterium glutamicum	99,367	29-Sep-97
rx02194	966	GB_BA1:ECOLW83	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,651	17-Apr-86
		GB_BA2:AF050166	840	AF050166	Corynebacterium glutamicum ATP phosphoribosyltransferase (hisG) gene, complete cds.	Corynebacterium glutamicum	98,214	5-Jan-99
rx02195	393	GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	93,805	6-Feb-99
		GB_PAT:E08649	188	E08649	DNA encoding part of aspartase from coryneform bacteria.	Corynebacterium glutamicum	100,000	29-Sep-97
		GB_BA2:AF086704	264	AF086704	Corynebacterium glutamicum phosphoribosyl-ATP-pyrophosphohydrolase (hisE) gene, complete cds.	Corynebacterium glutamicum	100,000	8-Feb-99
rx02198	2599	GB_BA1:EAY17145	6019	Y17145	Eubacterium acidaminophilum grdR, grdI, grdH genes and partial ldc, grdT genes.	Eubacterium acidaminophilum	39,075	5-Aug-98
rx02197	551	GB_STS:G01195	332	G01195	fruit fly STS Dm1930 clone DS06959 T7.	Drosophila melanogaster	35,542	28-Feb-95
		GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	33,938	17-Jun-98
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,517	27-Aug-99
		GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	36,770	01-MAR-1994
		GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	38,674	01-MAR-1994
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,465	27-Aug-98
rx02208	1025	GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	37,577	17-Jun-98
		GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	59,823	01-MAR-1994
		GB_BA1:AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 67.	Aeropyrum pernix	39,442	22-Jun-99
rx02229	648	GB_PR3:AC006236	127593	AC006236	Homo sapiens chromosome 17, clone hCT.162.E_12, complete sequence.	Homo sapiens	37,191	29-DEC-1998
		GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	63,541	03-DEC-1998
		GB_BA1:MTCY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	40,407	17-Jun-98
		GB_BA1:U00019	36033	U00019	Mycobacterium leprae cosmid B2235.	Mycobacterium leprae	40,541	01-MAR-1994
rx02234	3462	GB_BA1:U00019	36033	U00019	Mycobacterium leprae cosmid B2235.	Mycobacterium leprae	66,027	15-Jun-98
		GB_BA1:MSG8937CS	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	66,027	15-Jun-98
		GB_BA1:MTCY2512	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	71,723	18-Jun-98
		GB_BA2:U01072	4393	U01072	Mycobacterium bovis BCG orotidine-5-monophosphate decarboxylase (uraA) gene.	Mycobacterium bovis	67,101	22-DEC-1983

TABLE 4: ALIGNMENT RESULTS

rx02235	727	GB_BA1:MSU81572	980	U91572	Mycobacterium smegmatis carboxylate synthetase (pyrAB) gene, partial cds and oritidine 5'-monophosphate decarboxylase (pyrF) gene, complete cds.	Mycobacterium smegmatis	60,870	22-MAR-1997
		GB_HTC3:AC009364	192791	AC009364	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***	Homo sapiens	37,994	1-Sep-99
		GB_HTC3:AC009364	192791	AC009364	unordered pieces.	Homo sapiens	37,994	1-Sep-99
rx02237	693	GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	55,844	23-Jun-98
		GB_BA2:AF077324	5228	AF077324	Rhodococcus equi strain 103 plasmid RE-VP1 fragment f.	Rhodococcus equi	41,185	5-Nov-98
		GB_EST22:AU017763	586	AU017763	Mus musculus cDNA clone	Mus musculus	38,616	19-OCT-1998
rx02239	1389	GB_BA1:MTCY21B4	39150	Z80108	J0744A04 3', mRNA sequence.	Mycobacterium tuberculosis	56,282	23-Jun-98
		GB_HTC3:AC010745	193862	AC010745	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Homo sapiens	36,772	21-Sep-99
		GB_HTC3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,772	21-Sep-99
rx02240	1344	EM_PAT:E09855	1239	E09855	unordered pieces.	Corynebacterium glutamicum	99,515	07-OCT-1997 (Rel. 52, Created)
		GB_PAT:A37831	5392	A37831	gDNA encoding S-adenosylmethionine synthetase.	Streptomyces pristinaespiralis	83,568	05-MAR-1997
rx02248	1107	GB_BA2:AF117274	2303	AF117274	Sequence 1 from Patent WO9408014.	Streptomyces spectabilis	65,000	31-MAR-1999
		EM_BA1:AB003693	5589	AB003693	Streptomyces spectabilis flavoprotein homolog Dfp (dtp) gene, partial cds; and S-adenosylmethionine synthetase (metK) gene, complete cds.	Corynebacterium ammoniagenes	52,909	03-OCT-1997 (Rel. 52, Created)
		GB_PAT:E07957	5589	E07957	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	52,909	29-Sep-97
		GB_PAT:132742	5589	132742	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Unknown.	52,909	6-Feb-97
		GB_PAT:132743	2689	132743	Sequence 1 from patent US 5589355.	Unknown.	57,937	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Sequence 2 from patent US 5589355.	Corynebacterium ammoniagenes	57,937	03-OCT-1997 (Rel. 52, Created)
rx02249	600	GB_PAT:132742	5589	132742	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Unknown.	57,937	6-Feb-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	61,843	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	61,843	03-OCT-1997 (Rel. 52, Created)
		GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	61,843	29-Sep-97
		GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	64,348	29-Sep-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	64,348	6-Feb-97
		GB_PAT:132743	2689	132743	Sequence 2 from patent US 5589355.	Unknown.	64,348	6-Feb-97

TABLE 4: ALIGNMENT RESULTS

rx02250	643	GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	56,318	29-Sep-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	56,318	8-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	56,318	03-OCT-1987 (Rel. 52, Created)
rx02282	1269	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGAMTGENE	2028	X93513	C. glutamicum amt gene.	Corynebacterium glutamicum	100,000	29-MAY-1988
		GB_Vi:HEHCMVCG	229354	X17403	Human cytomegalovirus strain AD169 complete genome.	human herpesvirus 5	38,651	10-Feb-99
rx02283	488	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	37,526	7-Jan-99
rx02272	1368	EM_PAT:E09373	1591	E09373	Creatinine deiminase gene.	Bacillus sp.	96,928	08-OCT-1987 (Rel. 52, Created)
		GB_BA1:D38505	1591	D38505	Bacillus sp. gene for creatinine deaminase, complete cds.	Bacillus sp.	96,781	7-Aug-98
		GB_HTG2:AC006595	146070	AC006595	Homo sapiens, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,264	20-Feb-99
rx02281	1545	GB_GSS12:AQ411010	551	AQ411010	HS_2257_B1_H02_MR CIT Approved Human Genomic Sperm Library D	Homo sapiens	36,197	17-MAR-1999
		GB_EST23:AI128623	363	AI128623	Homo sapiens genomic clone Plate=2257 Col=3 Row=P, genomic survey sequence.	Homo sapiens	37,017	05-OCT-1998
		GB_PL2:ATAC007019	102335	AC007019	IMAGE:1691328 3', mRNA sequence.	Homo sapiens	33,988	18-MAR-1999
rx02299	531	GB_BA2:AF116184	540	AF116184	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence.	Arabidopsis thaliana	100,000	02-MAY-1999
		GB_GSS9:AQ164310	507	AQ164310	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds.	Corynebacterium glutamicum	37,278	16-OCT-1998
		GB_Vi:MH68TKH	4557	X93468	Homo sapiens genomic clone Plate=2171 Col=2 Row=L, genomic survey sequence.	Homo sapiens	40,288	3-Sep-96
rx02311	813	GB_HTG4:AC006091	176878	AC006091	Murine herpesvirus type 68 thymidine kinase and glycoprotein H genes.	murine herpesvirus 68	36,454	27-OCT-1999
		GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98	Drosophila melanogaster	36,454	27-OCT-1999
		GB_HTG4:AC006091	176878	AC006091	48.G.5 map 91F1-91F13 strain y; on bw sp. *** SEQUENCING IN PROGRESS ***	Drosophila melanogaster	36,454	27-OCT-1999

TABLE 4: ALIGNMENT RESULTS

	GB_BA2:RRU65510	16259	U65510	Rhodospirillum rubrum	37,828	8-Apr-97
				cooX, cooU, cooH genes, iron sulfur protein (cooF) gene, carbon monoxide dehydrogenase (cooS) gene, carbon monoxide dehydrogenase accessory proteins (cooC, cooT, cooJ) genes, putative transcriptional activator (cooA) gene, nicotinate-nucleotide pyrophosphorylase (nadC) gene, complete cds, L-aspartate oxidase (nadB) gene, and alkyl hydroperoxide reductase (ahpC) gene, partial cds.		
rx02315	1752	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	49,418	03-DEC-1998
		40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	49,360	17-Jun-98
		40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	38,150	03-DEC-1996
rx02318	402	11083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***; 3 ordered pieces.	35,821	08-OCT-1989
		11083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***; 3 ordered pieces.	35,821	06-OCT-1989
		89234	AC011412	Homo sapiens chromosome 5 clone CIT978SKB_81K21, *** SEQUENCING IN PROGRESS ***; 3 ordered pieces.	38,181	06-OCT-1999
rx02319	1080	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	37,792	03-DEC-1986
		40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	37,792	17-Jun-98
		476	AI117213	ub63h02.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1395123 5'mRNA sequence.	35,084	2-Sep-98
rx02345	1320	2582	X91189	B.ammoniaenes purK and purE genes.	61,731	14-Jan-97
		42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	39,624	10-Feb-99
		42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	39,847	10-Feb-99
rx02350	618	2582	X91189	B.ammoniaenes purK and purE genes.	64,286	14-Jan-97
		129528	X94335	S.cerevisiae 130kb DNA fragment from chromosome XV.	38,617	15-Jul-97
		50984	X90518	S.cerevisiae DNA of 51 Kb from chromosome XV right arm.	38,617	1-Nov-95
rx02373	1038	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	58,123	29-Sep-97
		1853	I06030	Sequence 4 from Patent EP 0305608.	56,220	02-DEC-1994
		1853	I00836	Sequence 1 from Patent US 4758514.	56,220	21-MAY-1993
rx02375	1350	3005	U31230	Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (prpB) gene, complete cds, and (unkdh) gene, complete cds.	89,332	2-Aug-98
		169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***; 1 unordered pieces.	38,115	8-Sep-99
		169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***; 1 unordered pieces.	38,115	8-Sep-99
rx02380	777	41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	38,088	17-Jun-98
		120754	AC010658	Drosophila melanogaster chromosome 3L75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***; 78 unordered pieces.	35,817	18-OCT-1989
		120754	AC010658	Drosophila melanogaster chromosome 3L75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***; 78 unordered pieces.	35,817	18-OCT-1989

TABLE 4: ALIGNMENT RESULTS

rx02382	1419	GB_BA1:CGPROAGEN	1783	X82929	C.glutamicum proA gene.	Corynebacterium glutamicum	98,802	23-Jan-97
		GB_BA1:MTVCY428	26914	Z81451	Mycobacterium tuberculosis H37Rv complete genome; segment 107/162.	Mycobacterium tuberculosis	38,054	17-Jun-98
		GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Oba protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	98,529	2-Aug-98
rx02400	693	GB_BA1:CGACEA	2427	X75504	C.glutamicum aceA gene and thx genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
		GB_PAT:188191	2135	I86191	Sequence 3 from patent US 5700561.	Unknown.	100,000	10-Jun-98
		GB_PAT:113693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	100,000	28-Sep-95
rx02432	1098	GB_GSS15:AQ606842	574	AQ606842	HS_5404_B2_E07_T7A RPCH-11 Human Male BAC Library Homo sapiens genomic clone Plate=980 Col=14 Row=J, genomic survey sequence.	Homo sapiens	39,716	10-Jun-99
		GB_EST1:T05804	406	T05804	EST03693 Fetal brain, Stragene (cat#936206) Homo sapiens cDNA clone HFBDG83 similar to EST containing Alu repeat, mRNA sequence.	Homo sapiens	37,915	30-Jun-93
		GB_PL1:AB006899	77363	AB006899	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence.	Arabidopsis thaliana	35,526	20-Nov-99
rx02458	1413	GB_BA2:AF114233	1852	AF114233	Corynebacterium glutamicum 5-enolpyruvylshikimate 3-phosphate synthase (aroA) gene, complete cds.	Corynebacterium glutamicum	100,000	7-Feb-99
		GB_EST37:AW013061	578	AW013061	ODT-00333 Winter flourider ovary Pleuronectes americanus cDNA clone ODT-0033 5' similar to FRUCTOSE-BISPHOSPHATE ALDOLASE B (LIVER), mRNA sequence.	Pleuronectes americanus	39,175	10-Sep-99
rx02469	1554	GB_GSS15:AQ650027	728	AQ650027	Sheared DNA-5L2.TF Sheared DNA Trypanosoma brucei genomic clone	Trypanosoma brucei	39,281	22-Jun-99
		GB_BA1:MTVCY359	36021	Z83859	Sheared DNA-5L2, genomic survey sequence.	Mycobacterium tuberculosis	39,634	17-Jun-98
		GB_BA1:MLCB1788	39228	AL008609	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium leprae	59,343	27-Aug-99
		GB_BA1:SCAJ10601	4682	AJ010601	Mycobacterium leprae cosmid B1788.	Sireplomyces coelicolor	48,889	17-Sep-98
		GB_BA2:CGU31224	422	U31224	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Corynebacterium glutamicum	96,445	2-Aug-96
		GB_BA1:MTVCY20G9	37218	Z77162	Corynebacterium glutamicum (ppx) gene, partial cds.	Mycobacterium tuberculosis	59,429	17-Jun-98
		GB_BA1:SCE7	18811	AL049819	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Sireplomyces coelicolor	39,510	10-MAY-1999
rx02489	933	GB_BA2:CGU31225	1817	U31225	Streptomyces coelicolor cosmid E7.	Corynebacterium glutamicum	97,749	2-Aug-98
		GB_BA1:NG17PILA	1920	X13965	Corynebacterium glutamicum L-proline:NADP+ 5-oxidoeductase (proC) gene, complete cds.	Neisseria gonorrhoeae	43,249	30-Sep-93
		GB_HTG2:AC007984	129715	AC007984	Neisseria gonorrhoeae pIIA gene.	Drosophila melanogaster	33,406	2-Aug-98
rx02501	1188	GB_BA1:MTVCY20G9	37218	Z77162	Drosophila melanogaster chromosome 3 clone BACR05C10 (D781) RPCL-98 05.C.10 map 97D-97E strain Y; on bw sp, *** SEQUENCING IN PROGRESS	Mycobacterium tuberculosis	39,357	17-Jun-98
		GB_BA1:U00018	42991	U00018	***, 87 unordered pieces.	Mycobacterium leprae	51,768	01-MAR-1994
		GB_VI:HE1CG	152261	X14112	Mycobacterium leprae cosmid B2168.	human herpesvirus 1	39,378	17-Apr-97
rx02503	522	GB_PR3:AC005328	35414	AC005328	Herpes simplex virus (HSV) type 1 complete genome.	Homo sapiens	39,922	28-Jul-98
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	39,922	3-Sep-98
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Homo sapiens	34,911	28-Jul-98
rx02504	681	GB_BA1:MTVCY20G9	37218	Z77162	Homo sapiens chromosome 19, cosmid R26680, complete sequence.	Mycobacterium tuberculosis	54,940	17-Jun-98
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	41,285	28-Jul-98
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Homo sapiens	41,265	3-Sep-98
rx02516	1388	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	37,723	04-DEC-1998



TABLE 4: ALIGNMENT RESULTS

rx02517	570	GB_BA1:U00013 GB_BA1:MTV007 GB_BA1:MLCL536 GB_BA1:U00013 GB_BA1:SCC22 GB_OV:AF137219 GB_EST30:AI645057	35881 32806 36224 35881 22115 831 301	U00013 AL021184 Z99125 U00013 AL086839 AF137219 AI645057	Mycobacterium leprae cosmid B1496. Mycobacterium tuberculosis H37Rv complete genome; segment 64/162. Mycobacterium leprae cosmid L536. Mycobacterium leprae cosmid B1496. Sireptomycetes coelicolor cosmid C22. Anlia calva mixed lineage leukemia-like protein (Mli) gene, partial cds. vs52a10.y1 Stralagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	37,723 61,335 37,018 37,018 37,071 36,853 41,860	Mycobacterium leprae Mycobacterium tuberculosis Mycobacterium leprae Mycobacterium leprae Sireptomycetes coelicolor Anlia calva Mus musculus	01-MAR-1994 17-Jun-98 04-DEC-1998 01-MAR-1994 12-Jul-99 7-Sep-99 28-Apr-99
rx02532	1170	GB_EST20:AA822595 GB_EST20:AA822595 GB_HTG2:AF130866 GB_HTG2:AF130866 GB_PL1:ATT12J5	429 429 118874 118874 84499	AA822595 AA822595 AF130866 AF130866 AL035522	Mus musculus vs52a10.r1 Stralagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence. Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS ***. In unordered pieces. Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS ***. In unordered pieces.	42,353 40,754 40,754 35,063	Mus musculus Homo sapiens Homo sapiens Arabidopsis thaliana	17-Feb-98 21-MAR-1999 21-MAR-1999 24-Feb-99
rx02550	1434	GB_BA1:MTCV279 GB_BA1:MSG81970CS GB_BA2:SC2H4	9150 39389 25970	Z97981 L78815 AL031514	Mycobacterium tuberculosis H37Rv complete genome; segment 17/162. Mycobacterium leprae cosmid B1970 DNA sequence. Sireptomycetes coelicolor cosmid 2H4.	37,773 39,024 37,906	Mycobacterium tuberculosis Mycobacterium leprae Sireptomycetes coelicolor A3(2)	17-Jun-98 15-Jun-98 19-OCT-1999
rx02559	1026	GB_BA1:MTV004 GB_PAT:128684 GB_BA1:MTU27357	69350 5100 5100	AL009198 I28684 U27357	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162. Sequence 1 from patent US 5573915. Mycobacterium tuberculosis cyclopropane mycolic acid synthase (cma1) gene, complete cds.	47,358 39,138 39,138	Mycobacterium tuberculosis Unknown. Mycobacterium tuberculosis	18-Jun-98 6-Feb-97 28-Sep-95
rx02622	1683	GB_BA2:AE001780 GB_OV:AF064564 GB_OV:AF064564	11997 49254 49254	AE001780 AF064564 AF064564	Thermotoga maritima section 92 of 136 of the complete genome. Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds. Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	44,814 39,732 36,703	Thermotoga maritima Fugu rubripes Fugu rubripes	2-Jun-99 17-Aug-99 17-Aug-99
rx02623	714	GB_GSS5:AQ818728 GB_HTG5:AC011083 GB_GSS6:AQ826948	444 195586 544	AQ818728 AC011083 AQ826948	HS_5268_A1_G09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=844 Col=17 Row=M, genomic survey sequence. Homo sapiens chromosome 9 clone RP11-111M7 map 9, WORKING DRAFT SEQUENCE, 51 unordered pieces. HS_5014_A2_C12_TTA RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=590 Col=24 Row=E, genomic survey sequence.	38,801 35,714 39,146	Homo sapiens Homo sapiens Homo sapiens	26-Aug-99 19-Nov-99 27-Aug-99
rx02629	708	GB_VI:BRSMGP GB_VI:BRSMGP	462 462	M86552 M86552	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds. Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	37,013 37,013	Bovine respiratory syncytial virus Bovine respiratory syncytial virus	28-Apr-93 28-Apr-93

TABLE 4: ALIGNMENT RESULTS

rx02845	1953	GB_PAT:A45577	1925	A45577	Sequence 1 from Patent WO9519442.	Corynebacterium glutamicum	39,130	07-MAR-1997
		GB_PAT:A45581	1925	A45581	Sequence 5 from Patent WO9519442.	Corynebacterium glutamicum	39,130	07-MAR-1997
		GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds.	Corynebacterium glutamicum	39,130	28-Apr-93
rx02846	1392	GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds.	Corynebacterium glutamicum	99,138	26-Apr-93
		GB_PAT:A45585	1925	A45585	Sequence 9 from Patent WO9519442.	Corynebacterium glutamicum	99,066	07-MAR-1997
		GB_PAT:A45583	1925	A45583	Sequence 7 from Patent WO9519442.	Corynebacterium glutamicum	99,066	07-MAR-1997
rx02848	1326	GB_OV:ICTCNC	2049	M83111	Ictidurus punctatus cyclic nucleotide-gated channel RNA sequence.	Ictidurus punctatus	38,402	24-MAY-1993
		GB_EST11:AA265464	345	AA265464	mx91c06.r1 Soares mouse N1ML Mus musculus cDNA clone IMAGE:693706	Mus musculus	38,655	20-MAR-1997
		GB_GSSB AQ008950	480	AQ008950	5' mRNA sequence.	Homo sapiens	38,074	27-Jun-98
rx02853					CIT-HSP-2294E14 TR CIT-HSP Homo sapiens genomic clone 2294E14, genomic survey sequence.			
rx02887	1068	GB_BA1:CORPHEA	1088	M13774	C glutamicum proA gene encoding prephenate dehydratase, complete cds.	Corynebacterium glutamicum	99,715	28-Apr-93
		GB_PAT:E04483	948	E04483	DNA encoding prephenate dehydratase	Corynebacterium glutamicum	98,523	29-Sep-97
		GB_PAT:E06110	948	E08110	DNA encoding prephenate dehydratase.	Corynebacterium glutamicum	98,523	29-Sep-97
rx02717	1005	GB_PL1:HVC4H	59748	Y14573	Hordeum vulgare DNA for chromosome 4H.	Hordeum vulgare	38,583	25-MAR-1999
		GB_PR2:HS10H5	29718	Z69705	Human DNA sequence from cosmid 310H5 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains EST and CpG island.	Homo sapiens	38,089	22-Nov-99
		GB_PR3:AC004754	39188	AC004754	Homo sapiens chromosome 16, cosmid clone RT286 (LANL), complete sequence.	Homo sapiens	36,089	28-MAY-1998
rx02754	1461	GB_HTG2:AC008223	130212	AC008223	Drosophila melanogaster chromosome 3 clone BACR16118 (DB15) RPCI-98	Drosophila melanogaster	32,757	2-Aug-99
		GB_HTG2:AC008223	130212	AC008223	16.1.18 map 95A-95A strain y; cn bw sp. *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	32,757	2-Aug-99
rx02758	1422	GB_BA1:MTCY71	42729	Z92771	Drosophila melanogaster chromosome 3 clone BACR16118 (DB15) RPCI-98	Drosophila melanogaster	37,838	10-Feb-99
		GB_HTG5:AC011678	171967	AC011678	16.1.18 map 95A-95A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***, 101 unordered pieces.	Mycobacterium tuberculosis	35,331	5-Nov-99
		GB_HTG5:AC011678	171967	AC011678	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Homo sapiens	33,807	5-Nov-99
		GB_BA2:AF064070	23183	AF064070	Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS ***; 20 unordered pieces.	Burkholderia pseudomallei	36,929	20-Jan-99
					Burkholderia pseudomallei putative dihydroorotase (pyrC) gene, partial cds; putative 1-acyl-sn-glycerol-3-phosphate acyltransferase (plsC), putative diadenosine tetraphosphate (apaH), complete cds; type II O-antigen biosynthesis gene cluster, complete sequence; putative undecaprenyl phosphate N-acetylglucosaminyltransferase, and putative UDP-glucose 4-epimerase genes, complete cds; and putative galactosyl transferase gene, partial cds.			

TABLE 4: ALIGNMENT RESULTS

rx02771	678	GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dcIAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene	Corynebacterium glutamicum	99,852	14-Sep-88
		GB_IN1:CELT1984	37121	U30438	<i>Caenorhabditis elegans</i> contig T1984	<i>Caenorhabditis elegans</i>	43,838	04-DEC-1996
		GB_EST36:AV193572	360	AV193572	AV193572 Y.u. Kohara unpublished cDNA Strain N2 hermaphrodite embryo	<i>Caenorhabditis elegans</i>	48,568	22-Jul-99
rx02772	1158	GB_BA2:AF038651	4077	AF038651	<i>Caenorhabditis elegans</i> cDNA clone YK618h8.5, mRNA sequence	Corynebacterium glutamicum	99,914	14-Sep-98
		GB_BA1:MTCY227	35946	Z77724	Corynebacterium glutamicum dipeptide-binding protein (dcIAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene	Mycobacterium tuberculosis	38,339	17-Jun-98
		GB_BA1:U00011	40429	U00011	Mycobacterium tuberculosis H37Rv complete genome; segment 114/162	Mycobacterium leprae	38,996	01-MAR-1994
rx02780	1266	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162	Mycobacterium tuberculosis	37,640	17-Jun-98
		GB_PR3:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC11-259018 (Roswell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	37,906	3-Jun-99
		GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC11-259018 (Roswell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	35,280	3-Jun-99
rx02791	951	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162	Mycobacterium tuberculosis	39,765	17-Jun-98
		GB_OV:CHKCEK2	3684	M35195	Chicken tyrosine kinase (ck2) mRNA, complete cds	Gallus gallus	38,937	28-Apr-83
		GB_BA1:MSASDASK	5037	Z17372	M. smegmatis asd, ask-alpha, and ask-beta genes	Mycobacterium smegmatis	38,495	9-Aug-94
rx02802	1194	GB_EST24:AI223401	169	AI223401	qj48g01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394.; mRNA sequence	Homo sapiens	40,828	27-OCT-1998
		GB_EST24:AI223401	169	AI223401	qj48g01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394.; mRNA sequence	Homo sapiens	40,828	27-OCT-1998
rx02814	494	GB_BA1:MTCY7D11	22070	Z95120	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162	Mycobacterium tuberculosis	58,418	17-Jun-98
		GB_BA1:MTCY7D11	22070	Z95120	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162	Mycobacterium tuberculosis	40,496	17-Jun-98
		GB_PR1:HSJA2962	778	AJ002962	Homo sapiens mRNA for hB-FABP	Homo sapiens	39,828	8-Jan-98
rx02843	608	GB_BA1:CGAJ4934	1180	AJ004934	Corynebacterium glutamicum dapD gene, complete CDS	Corynebacterium glutamicum	100,000	17-Jun-98
		GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162	Mycobacterium tuberculosis	37,710	17-Jun-98
		GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid B1756	Mycobacterium leprae	39,628	09-MAR-1995
rx03205	863	GB_BA1:BLSIGBGN	2906	Z49824	B.lactofermentum orf1 gene and sigB gene	Corynebacterium glutamicum	98,854	26-Apr-86
		GB_EST21:AA980237	377	AA980237	IMAGE:1348414 5' similar to TR:Q61025 Q61025 HYPOTHETICAL 15.2 KD PROTEIN.; mRNA sequence	Mus musculus	41,489	27-MAY-1998
		GB_EST23:AI156316	371	AI156316	ud27c05.r1 Soares_thymus_2NbMT Mus musculus cDNA clone	Mus musculus	38,005	30-Sep-88
		GB_IN1:LMFL2743	38368	AL031910	IMAGE:1447112 5' mRNA sequence	Leishmania major	39,869	15-DEC-1989
rx03223	1237	GB_PR3:HSDJ6182	119666	AL096710	Leishmania major Friedlin chromosome 4 cosmid L2743. Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STSs and GSSs, complete sequence	Homo sapiens	34,930	17-DEC-1989

TABLE 4: ALIGNMENT RESULTS

GB_PR3:HSDJ61B2	119668	AL096710	Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STSs and GSSs, complete sequence.	34,634	17-DEC-1999
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What is claimed:

1. 1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a metabolic pathway protein selected from the group consisting of a nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5.
2. The isolated nucleic acid molecule of claim 1, wherein said metabolic pathway protein is involved in the metabolism of an amino acid.
3. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6.
4. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence set forth in SEQ ID NO:6, or a complement thereof.
5. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 65% homologous to a nucleotide sequence set forth in SEQ ID NO:1, or a complement thereof.
6. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth set forth in SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5.
7. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-6 under stringent conditions.
8. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1, or a portion thereof, and a nucleotide sequence encoding a heterologous polypeptide.
9. A vector comprising the nucleic acid molecule of claim 1.
10. The vector of claim 9, further comprising one or more metabolic pathway nucleic acid molecules.
11. The vector of claim 9 or 10, which is an expression vector.

12. A host cell transfected with the expression vector of claim 9 or 10.
13. The vector of claim 10, wherein the second metabolic pathway nucleic acid  
5 molecule is selected from the group consisting of a nucleic acid molecule  
comprising the nucleotide sequence set forth in the odd-numbered sequences listed  
in Table 1, excluding any F-designated nucleic acid molecules.
14. The host cell of claim 12, wherein said cell is a microorganism.
- 10 15. The host cell of claim 12, wherein said cell belongs to the genus *Corynebacterium*  
or *Brevibacterium*.
16. The host cell of claim 12, wherein the expression of said nucleic acid molecules  
15 results in the modulation in production of a fine chemical from said cell.
17. The host cell of claim 16, wherein said fine chemical is an amino acid.
18. The host cell of claim 17, wherein said amino acid is methionine or lysine.
- 20 19. A method of producing a polypeptide comprising culturing the host cell of claim 12  
in an appropriate culture medium to, thereby, produce the polypeptide.
20. An isolated metabolic pathway polypeptide from *Corynebacterium glutamicum*, or a  
25 portion thereof.
21. The protein of claim 20, wherein said polypeptide is selected from the group of  
metabolic pathway proteins which participate in the metabolism of an amino acid.
- 30 22. The protein of claim 21, wherein said amino acid is methionine or lysine.
23. An isolated nucleic acid molecule from *Corynebacterium glutamicum* which  
encodes a metabolic pathway protein comprising the amino acid sequence set forth  
in SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6.
- 35 24. An isolated polypeptide comprising a naturally occurring allelic variant of a  
polypeptide comprising an amino acid sequence selected from the group consisting  
of those sequences set forth in SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6.

25. The isolated polypeptide of claim 23, further comprising heterologous amino acid sequences.
- 5 26. An isolated polypeptide comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence set forth in SEQ ID NO:5, or a complement thereof.
- 10 27. An isolated polypeptide comprising a nucleotide sequence which is at least 65% homologous to a nucleotide sequence set forth in SEQ ID NO:1, or a complement thereof.
- 15 28. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 9 or 10, such that the fine chemical is produced.
- 20 29. The method of claim 28, wherein said cell is cultured in the presence of a sulfur source.
30. The method of claim 28, wherein said method further comprises the step of recovering the fine chemical from said culture.
31. The method of claim 28, wherein said fine chemical is an amino acid.
32. The method of claim 31, wherein said amino acid is methionine or lysine.
- 25 33. The method of claim 28, wherein said method further comprises the step of transfecting said cell with the vector of claim 9 or 10, to result in a cell containing said vector.
- 30 34. The method of claim 28, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
- 35 35. The method of claim 27, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium*

- fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*,  
*Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*,  
*Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium*  
*ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*,  
5 *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.

36. A method for producing a fine chemical, comprising culturing a cell whose genomic  
DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims  
10 1-6.

37. A method for producing a fine chemical, comprising culturing a cell whose genomic  
DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims  
1-6, alone or in combination with another metabolic pathway nucleic acid selected from  
15 the group consisting of a nucleic acid molecule comprising the nucleotide sequence set  
forth in the odd-numbered sequences listed in Table 1, excluding any F-designated  
nucleic acid molecules.

38. A method for producing a fine chemical, comprising culturing a cell whose genomic  
20 DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims  
1-6, alone or in combination with one or more metabolic pathway nucleic acid molecule.

39. The method of claim 36, wherein the metabolic pathway nucleic acid molecule is  
selected from the group consisting of *metZ*, *metC*, *metB*, *metA*, *metE*, *metH*, *hom*, *asd*,  
25 *lysC*, *lysC/ask*, *rxn00657*, *dapA*, *dapB*, *dapC*, *dapD/argD*, *dapE*, *dapF*, *lysA*, *ddh*, *lysE*,  
*lysG*, *lysR*, *hsk*, *ppc*, *pycA*, *accD*, *accA*, *accB*, *accC*, *gpdh* genes encoding glucose-6-  
phosphate-dehydrogenase, *opcA*, *pgdh*, *ta*, *tk*, *pgl*, *rlpe*, *rpe* or any combination of the  
above-mentioned genes.

40. The method of claim 35 or 36, wherein said metabolic pathway is methionine or  
lysine metabolism.



41. A method of modulating the yield of a fine chemical from a cell comprising, introducing one or more metabolic pathway genes into a cell, thereby modulating the yield of a fine chemical.

5 42. The method of claim 41, wherein said metabolic pathway gene or genes are integrated into the chromosome of the cell.

43. The method of claim 41, wherein said metabolic pathway gene or genes are maintained on a plasmid.

10

44. The method of claim 41, wherein said fine chemical is an amino acid.

45. The method of claim 44, wherein said amino acid is methionine or lysine.

15 46. The method of claim 41, wherein said metabolic pathway gene or genes are selected from the group consisting of the nucleic acid molecule of any one of claims 1-6.

47. The method of claim 41, wherein the nucleotide sequence of said metabolic pathway gene or genes has been mutated to increase yield of a fine chemical.

20

## SEQUENCE LISTING

&lt;110&gt; BASF Aktiengesellschaft

<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
METABOLIC PATHWAY PROTEINS

&lt;130&gt; BGI-121CP2PC

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; 09/606740

&lt;151&gt; 2000-06-23

&lt;150&gt; 60/187970

&lt;151&gt; 2000-03-09

&lt;160&gt; 125

&lt;170&gt; PatentIn Vers. 2.0

&lt;210&gt; 1

&lt;211&gt; 1840

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (363)..(1676)

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aagctgttca gtaggggtgca tgggagaaga atttcctaataaaaaactctt aaggacctcc 360

aa atg cca aag tac gac aat tcc aat gct gac cag tgg ggc ttt gaa 407
  Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu
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Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala
          20          25          30

cga aac ctt ccg atc tac caa tcc acc gct ttc gtg ttc gac tcc gct 503
Arg Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala
          35          40          45

gag cac gcc aag cag cgt ttc gca ctt gag gat cta ggc cct gtt tac 551
Glu His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr
          50          55          60

tcc cgc ctc acc aac cca acc gtt gag gct ttg gaa aac cgc atc gct 599

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Ser	Arg	Leu	Thr	Asn	Pro	Thr	Val	Glu	Ala	Leu	Glu	Asn	Arg	Ile	Ala	
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tcc	ctc	gaa	ggt	ggc	gtc	cac	gct	gta	gcg	ttc	tcc	tcc	gga	cag	gcc	647
Ser	Leu	Glu	Gly	Gly	Val	His	Ala	Val	Ala	Phe	Ser	Ser	Gly	Gln	Ala	
80					85					90					95	
gca	acc	acc	aac	gcc	att	ttg	aac	ctg	gca	gga	gcg	ggc	gac	cac	atc	695
Ala	Thr	Thr	Asn	Ala	Ile	Leu	Asn	Leu	Ala	Gly	Ala	Gly	Asp	His	Ile	
			100						105					110		
gtc	acc	tcc	cca	cgc	ctc	tac	ggt	ggc	acc	gag	act	cta	ttc	ctt	atc	743
Val	Thr	Ser	Pro	Arg	Leu	Tyr	Gly	Gly	Thr	Glu	Thr	Leu	Phe	Leu	Ile	
			115					120					125			
act	ctt	aac	cgc	ctg	ggt	atc	gat	gtt	tcc	ttc	gtg	gaa	aac	ccc	gac	791
Thr	Leu	Asn	Arg	Leu	Gly	Ile	Asp	Val	Ser	Phe	Val	Glu	Asn	Pro	Asp	
		130					135					140				
gac	cct	gag	tcc	tgg	cag	gca	gcc	gtt	cag	cca	aac	acc	aaa	gca	ttc	839
Asp	Pro	Glu	Ser	Trp	Gln	Ala	Ala	Val	Gln	Pro	Asn	Thr	Lys	Ala	Phe	
	145					150					155					
ttc	ggc	gag	act	ttc	gcc	aac	cca	cag	gca	gac	gtc	ctg	gat	att	cct	887
Phe	Gly	Glu	Thr	Phe	Ala	Asn	Pro	Gln	Ala	Asp	Val	Leu	Asp	Ile	Pro	
160					165					170					175	
gcg	gtg	gct	gaa	gtt	gcg	cac	cgc	aac	agc	gtt	cca	ctg	atc	atc	gac	935
Ala	Val	Ala	Glu	Val	Ala	His	Arg	Asn	Ser	Val	Pro	Leu	Ile	Ile	Asp	
				180					185					190		
aac	acc	atc	gct	acc	gca	gcg	ctc	gtg	cgc	ccg	ctc	gag	ctc	ggc	gca	983
Asn	Thr	Ile	Ala	Thr	Ala	Ala	Leu	Val	Arg	Pro	Leu	Glu	Leu	Gly	Ala	
			195					200					205			
gac	gtt	gtc	gtc	gct	tcc	ctc	acc	aag	ttc	tac	acc	ggc	aac	ggc	tcc	1031
Asp	Val	Val	Val	Ala	Ser	Leu	Thr	Lys	Phe	Tyr	Thr	Gly	Asn	Gly	Ser	
		210					215					220				
gga	ctg	ggc	ggc	gtg	ctt	atc	gac	ggc	gga	aag	ttc	gat	tgg	act	gtc	1079
Gly	Leu	Gly	Gly	Val	Leu	Ile	Asp	Gly	Gly	Lys	Phe	Asp	Trp	Thr	Val	
	225					230					235					
gaa	aag	gat	gga	aag	cca	gta	ttc	ccc	tac	ttc	gtc	act	cca	gat	gct	1127
Glu	Lys	Asp	Gly	Lys	Pro	Val	Phe	Pro	Tyr	Phe	Val	Thr	Pro	Asp	Ala	
240					245					250					255	
gct	tac	cac	gga	ttg	aag	tac	gca	gac	ctt	ggt	gca	cca	gcc	ttc	ggc	1175
Ala	Tyr	His	Gly	Leu	Lys	Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	Phe	Gly	
				260					265					270		
ctc	aag	gtt	cgc	gtt	ggc	ctt	cta	cgc	gac	acc	ggc	tcc	acc	ctc	tcc	1223
Leu	Lys	Val	Arg	Val	Gly	Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	Leu	Ser	
			275					280					285			
gca	ttc	aac	gca	tgg	gct	gca	gtc	cag	ggc	atc	gac	acc	ctt	tcc	ctg	1271
Ala	Phe	Asn	Ala	Trp	Ala	Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	Ser	Leu	
		290					295					300				
cgc	ctg	gag	cgc	cac	aac	gaa	aac	gcc	atc	aag	gtt	gca	gaa	ttc	ctc	1319
Arg	Leu	Glu	Arg	His	Asn	Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu	Phe	Leu	

305	310	315	
aac aac cac gag aag gtg gaa aag gtt aac ttc gca ggc ctg aag gat			1367
Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu Lys Asp			
320	325	330	335
tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg aag tac acc ggc			1415
Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly			
	340	345	350
tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct tgg gca			1463
Ser Val Leu Thr Phe Glu Ile Lys Ser Gly Lys Asp Glu Ala Trp Ala			
	355	360	365
ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc ggc gat			1511
Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile Gly Asp			
	370	375	380
gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca cag tcc			1559
Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser			
	385	390	395
gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc gtc cgc			1607
Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr Val Arg			
	400	405	410
ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac ctc gaa			1655
Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu			
	420	425	430
ggc ggc ttt gct gca atc tag ctttaaataag actcacccca gtgcttaaag			1706
Gly Gly Phe Ala Ala Ile			
	435		
cgctggggttt ttctttttca gactcgtgag aatgcaaact agactagaca gagctgtcca			1766
tatacactgg acgaagtttt agtcttgtcc acccagaaca ggcggttatt ttcattgccca			1826
ccctcgcgcc ttca			1840

&lt;210&gt; 2

&lt;211&gt; 437

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 2

Met	Pro	Lys	Tyr	Asp	Asn	Ser	Asn	Ala	Asp	Gln	Trp	Gly	Phe	Glu	Thr
1				5				10						15	
Arg	Ser	Ile	His	Ala	Gly	Gln	Ser	Val	Asp	Ala	Gln	Thr	Ser	Ala	Arg
			20					25					30		
Asn	Leu	Pro	Ile	Tyr	Gln	Ser	Thr	Ala	Phe	Val	Phe	Asp	Ser	Ala	Glu
		35					40					45			
His	Ala	Lys	Gln	Arg	Phe	Ala	Leu	Glu	Asp	Leu	Gly	Pro	Val	Tyr	Ser
	50					55					60				
Arg	Leu	Thr	Asn	Pro	Thr	Val	Glu	Ala	Leu	Glu	Asn	Arg	Ile	Ala	Ser
65					70					75					80

Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Scr Gly Gln Ala Ala  
 85 90 95  
 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val  
 100 105 110  
 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr  
 115 120 125  
 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp  
 130 135 140  
 Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe  
 145 150 155 160  
 Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro Ala  
 165 170 175  
 Val Ala Glu Val Ala His Arg Asn Ser Val Pro Leu Ile Ile Asp Asn  
 180 185 190  
 Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala Asp  
 195 200 205  
 Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser Gly  
 210 215 220  
 Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe Asp Trp Thr Val Glu  
 225 230 235 240  
 Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val Thr Pro Asp Ala Ala  
 245 250 255  
 Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu  
 260 265 270  
 Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala  
 275 280 285  
 Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg  
 290 295 300  
 Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn  
 305 310 315 320  
 Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser  
 325 330 335  
 Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser  
 340 345 350  
 Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe  
 355 360 365  
 Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val  
 370 375 380  
 Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser Asp  
 385 390 395 400

Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu  
 405 410 415

Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly  
 420 425 430

Gly Phe Ala Ala Ile  
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<210> 3

<211> 1495

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (287)..(1264)

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gaagtgcgac ggctaacagg gctgggattg tcctcaactt cacttcgggc tccttcttag 120

taataggttc gtagaaaagt ttactagcct agagagtatg cgatttcctg aactcgaaga 180

attgaagaat cgccggacct tgaaatggac ccggtttcca gaagacgtgc ttcctttgtg 240

ggttgcggaa agtgattttg gcacctgccc gcagttgaag gaagct atg gca gat 295  
 Met Ala Asp  
 1

gcc gtt gag cgc gag gtc ttc gga tac cca cca gat gct act ggg ttg 343  
 Ala Val Glu Arg Glu Val Phe Gly Tyr Pro Pro Asp Ala Thr Gly Leu  
 5 10 15

aat gat gcg ttg act gga ttc tac gag cgt cgc tat ggg ttt ggc cca 391  
 Asn Asp Ala Leu Thr Gly Phe Tyr Glu Arg Arg Tyr Gly Phe Gly Pro  
 20 25 30 35

aat ccg gaa agt gtt ttc gcc att ccg gat gtg gtt cgt ggc ctg aag 439  
 Asn Pro Glu Ser Val Phe Ala Ile Pro Asp Val Val Arg Gly Leu Lys  
 40 45 50

ctt gcc att gag cat ttc act aag cct ggt tcg gcg atc att gtg ccg 487  
 Leu Ala Ile Glu His Phe Thr Lys Pro Gly Ser Ala Ile Ile Val Pro  
 55 60 65

ttg cct gca tac cct cct ttc att gag ttg cct aag gtg act ggt cgt 535  
 Leu Pro Ala Tyr Pro Pro Phe Ile Glu Leu Pro Lys Val Thr Gly Arg  
 70 75 80

cag gcg atc tac att gat gcg cat gag tac gat ttg aag gaa att gag 583  
 Gln Ala Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys Glu Ile Glu  
 85 90 95

aag gcc ttc gct gac ggt gcg gga tca ctg ttg ttc tgc aat cca cac 631  
 Lys Ala Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys Asn Pro His  
 100 105 110 115

aac cca ctg ggc acg gtc ttt tct gaa gag tac atc cgc gag ctc acc 679

Asn	Pro	Leu	Gly	Thr	Val	Phe	Ser	Glu	Glu	Tyr	Ile	Arg	Glu	Leu	Thr		
				120					125					130			
gat	att	gcg	gcg	aag	tac	gat	gcc	cgc	atc	atc	gtc	gat	gag	atc	cac	727	
Asp	Ile	Ala	Ala	Lys	Tyr	Asp	Ala	Arg	Ile	Ile	Val	Asp	Glu	Ile	His		
			135					140					145				
gcg	cca	ctg	gtt	tat	gaa	ggc	acc	cat	gtg	gtt	gct	gct	ggg	gtt	tct	775	
Ala	Pro	Leu	Val	Tyr	Glu	Gly	Thr	His	Val	Val	Ala	Ala	Gly	Val	Ser		
		150					155					160					
gag	aac	gct	gca	aac	act	tgc	atc	acc	atc	acc	gca	act	tct	aag	gcg	823	
Glu	Asn	Ala	Ala	Asn	Thr	Cys	Ile	Thr	Ile	Thr	Ala	Thr	Ser	Lys	Ala		
	165					170					175						
tgg	aac	act	gct	ggg	ttg	aag	tgt	gct	cag	atc	ttc	ttc	agt	aat	gaa	871	
Trp	Asn	Thr	Ala	Gly	Leu	Lys	Cys	Ala	Gln	Ile	Phe	Phe	Ser	Asn	Glu		
180					185					190					195		
gcc	gat	gtg	aag	gcc	tgg	aag	aat	ttg	tgc	gat	att	acc	cgt	gac	ggg	919	
Ala	Asp	Val	Lys	Ala	Trp	Lys	Asn	Leu	Ser	Asp	Ile	Thr	Arg	Asp	Gly		
				200					205					210			
gtg	tcc	atc	ctt	gga	ttg	atc	gct	gcg	gag	aca	gtg	tac	aac	gag	ggc	967	
Val	Ser	Ile	Leu	Gly	Leu	Ile	Ala	Ala	Glu	Thr	Val	Tyr	Asn	Glu	Gly		
			215					220					225				
gaa	gaa	ttc	ctt	gat	gag	tca	att	cag	att	ctc	aag	gac	aac	cgt	gac	1015	
Glu	Glu	Phe	Leu	Asp	Glu	Ser	Ile	Gln	Ile	Leu	Lys	Asp	Asn	Arg	Asp		
		230					235					240					
ttt	gcg	gct	gct	gaa	ctg	gaa	aag	ctt	ggc	gtg	aag	gtc	tac	gca	ccg	1063	
Phe	Ala	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Gly	Val	Lys	Val	Tyr	Ala	Pro		
	245					250					255						
gac	tcc	act	tat	ttg	atg	tgg	ttg	gac	ttc	gct	ggc	acc	aag	atc	gaa	1111	
Asp	Ser	Thr	Tyr	Leu	Met	Trp	Leu	Asp	Phe	Ala	Gly	Thr	Lys	Ile	Glu		
260					265				270					275			
gag	gcg	cct	tct	aaa	att	ctt	cgt	gag	gag	ggg	aag	gtc	atg	ctg	aat	1159	
Glu	Ala	Pro	Ser	Lys	Ile	Leu	Arg	Glu	Glu	Gly	Lys	Val	Met	Leu	Asn		
				280				285					290				
gat	ggc	gca	gct	ttt	ggg	ggg	ttc	acc	acc	tgc	gct	cgt	ctt	aat	ttt	1207	
Asp	Gly	Ala	Ala	Phe	Gly	Gly	Phe	Thr	Thr	Cys	Ala	Arg	Leu	Asn	Phe		
			295				300						305				
gcg	tgt	tcc	aga	gag	acc	ctt	gag	gag	ggg	ctg	cgc	cgt	atc	gcc	agc	1255	
Ala	Cys	Ser	Arg	Glu	Thr	Leu	Glu	Glu	Gly	Leu	Arg	Arg	Ile	Ala	Ser		
		310				315					320						
gtg	ttg	taa	ataatgagta	aaaagtctgt	cctgattact	tctttgatgc										1304	
Val	Leu																
		325															
tggttttccat	gttcttcgga	gctggaaacc	tcattctccc	gccgatgctt	ggattgtcgg											1364	
caggaaccaa	ctatctacca	gctatcttag	gatttctagc	aacgagtgtt	ctgctcccgg											1424	
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gcggtaagat c

1495

&lt;210&gt; 4

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 4

Met Ala Asp Ala Val Glu Arg Glu Val Phe Gly Tyr Pro Pro Asp Ala  
 1 5 10 15

Thr Gly Leu Asn Asp Ala Leu Thr Gly Phe Tyr Glu Arg Arg Tyr Gly  
 20 25 30

Phe Gly Pro Asn Pro Glu Ser Val Phe Ala Ile Pro Asp Val Val Arg  
 35 40 45

Gly Leu Lys Leu Ala Ile Glu His Phe Thr Lys Pro Gly Ser Ala Ile  
 50 55 60

Ile Val Pro Leu Pro Ala Tyr Pro Pro Phe Ile Glu Leu Pro Lys Val  
 65 70 75 80

Thr Gly Arg Gln Ala Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys  
 85 90 95

Glu Ile Glu Lys Ala Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys  
 100 105 110

Asn Pro His Asn Pro Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg  
 115 120 125

Glu Leu Thr Asp Ile Ala Ala Lys Tyr Asp Ala Arg Ile Ile Val Asp  
 130 135 140

Glu Ile His Ala Pro Leu Val Tyr Glu Gly Thr His Val Val Ala Ala  
 145 150 155 160

Gly Val Ser Glu Asn Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr  
 165 170 175

Ser Lys Ala Trp Asn Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe  
 180 185 190

Ser Asn Glu Ala Asp Val Lys Ala Trp Lys Asn Leu Ser Asp Ile Thr  
 195 200 205

Arg Asp Gly Val Ser Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr  
 210 215 220

Asn Glu Gly Glu Glu Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp  
 225 230 235 240

Asn Arg Asp Phe Ala Ala Ala Glu Leu Glu Lys Leu Gly Val Lys Val  
 245 250 255

Tyr Ala Pro Asp Ser Thr Tyr Leu Met Trp Leu Asp Phe Ala Gly Thr  
 260 265 270

Lys Ile Glu Glu Ala Pro Ser Lys Ile Leu Arg Glu Glu Gly Lys Val



	275						280						285					
Met	Leu	Asn	Asp	Gly	Ala	Ala	Phe	Gly	Gly	Phe	Thr	Thr	Cys	Ala	Arg			
	290					295					300							
Leu	Asn	Phe	Ala	Cys	Ser	Arg	Glu	Thr	Leu	Glu	Glu	Gly	Leu	Arg	Arg			
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Ile	Ala	Ser	Val	Leu														
				325														
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				Met Ser Thr Glu Asp	5													
att gtc gtc gta gca gta gat ggc tgc gac gcc tca aaa caa gct gtt	163																	
Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val	20																	
cgg tgg gct gca aat acc gcc aac aaa cgt ggc att cca ctt cgc ttg	211																	
Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu	35																	
gct tcc agc tac acc atg cct cag ttc ctg tac gca gag gga atg gtt	259																	
Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val	50																	
cca cca caa gag ctt ttc gat gac clc cag gcc gaa gcc ctg gaa aag	307																	
Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys	65																	
att aac gaa gcc cgt gac atc gcc cat gag gta gcg cca gaa atc aag	355																	
Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys	85																	
atc ggg cac acc atc gct gaa ggc agt ccc atc gac atg ctg ttg gaa	403																	
Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu	100																	
atg tct ccc gat gcc aca atg atc gtc atg ggt tcc cgc gga ctg ggc	451																	
Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly	115																	
gga ctg tcc gga atg gtc atg ggc tcc gtc tcc ggt gca gtg gtc agc	499																	
Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser	130																	
cac gca aag tgt cca gtc gtt gtt gtc cgt gaa gac agc gca gtc aac	547																	

His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn  
 135 140 145  
 gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa 595  
 Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu  
 150 155 160 165  
 gtc tcc caa cag gca acc gaa tac gca ttt gcg gaa gct gaa gct cgt 643  
 Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg  
 170 175 180  
 ggc gcc gaa ctg gtt gca gtt cac acc tgg atg gac atg cag gta cag 691  
 Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln  
 185 190 195  
 gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg 739  
 Ala Ser Leu Ala Gly Leu Ala Ala Gln Gln Gln Trp Asp Glu Val  
 200 205 210  
 gaa cgt cag caa acc gac atg ctg atc gaa cgc ctg gca cca ctg gtg 787  
 Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val  
 215 220 225  
 gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac cgc 835  
 Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg  
 230 235 240 245  
 cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctg cta gtc 883  
 Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val  
 250 255 260  
 gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc atg ctg ctt ggc tcc 931  
 Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser  
 265 270 275  
 acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt 979  
 Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val  
 280 285 290  
 cgc cca cct gag aag att aag aag tag tttcttttaa gtttcgatgc cccggtt 1033  
 Arg Pro Pro Glu Lys Ile Lys Lys  
 295 300

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 <212> PRT  
 <213> *Corynebacterium glutamicum*

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 Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr  
 35 40 45  
 Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala  
 50 55 60

Glu Ala L u Glu Lys Ile Asn Glu Ala Arg Asp Il Ala His Glu Val  
 65 70 75 80  
 Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile  
 85 90 95  
 Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly  
 100 105 110  
 Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser  
 115 120 125  
 Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu  
 130 135 140  
 Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly  
 145 150 155 160  
 Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala  
 165 170 175  
 Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met  
 180 185 190  
 Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln  
 195 200 205  
 Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg  
 210 215 220  
 Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile  
 225 230 235 240  
 Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn  
 245 250 255  
 Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly  
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 275 280 285  
 Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys  
 290 295 300

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 <212> DNA  
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<220>  
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 <222> (101) .. (925)  
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	Leu	Thr	Ile	Pro	Phe	
	1				5	
gcc aaa ggc cac gcc acc gaa aac gac ttc atc atc atc ccc gat gag 163 Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile Ile Ile Pro Asp Glu 10 15 20						
gat gcg cgc cta gat tta act cca gaa atg gtg gtc acg ctg tgt gac 211 Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val Val Thr Leu Cys Asp 25 30 35						
cgc cgc gcc ggg atc ggt gct gat ggt atc ctc cgc gtg gtt aaa gct 259 Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu Arg Val Val Lys Ala 40 45 50						
gca gac gta gaa ggc tcc acg gtc gac cca tcg ctg tgg ttc atg gat 307 Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser Leu Trp Phe Met Asp 55 60 65						
tac cgc aac gcc gat gga tct ttg gct gaa atg tgc ggc aat ggt gtg 355 Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met Cys Gly Asn Gly Val 70 75 80 85						
cgc ctg ttc gcg cac tgg ctg tac tcc cgc ggt ctt gtt gat aat acg 403 Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly Leu Val Asp Asn Thr 90 95 100						
agc ttt gat atc ggt acc cgc gcc ggt gtc cgc cac gtt gat att ttg 451 Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg His Val Asp Ile Leu 105 110 115						
cag gca gat caa cat tct gcg cag gtc cgc gtt gat atg ggc atc cct 499 Gln Ala Asp Gln His Ser Ala Gln Val Arg Val Asp Met Gly Ile Pro 120 125 130						
gac gtc acg gga tta tcc acc tgc gac atc aac ggc caa gta ttc gct 547 Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn Gly Gln Val Phe Ala 135 140 145						
ggc ctt ggc gtt gat atg ggt aac cca cac cta gcg tgc gtt gtg ccg 595 Gly Leu Gly Val Asp Met Gly Asn Pro His Leu Ala Cys Val Val Pro 150 155 160 165						
ggc tta agt gcg tcg gct ctt gcc gat atg gaa ctg cgc gca cct acg 643 Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu Leu Arg Ala Pro Thr 170 175 180						
ttt gat cag gaa ttc ttc ccc cac ggt gtg aac gta gaa atc gtc aca 691 Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn Val Glu Ile Val Thr 185 190 195						
gaa tta gaa gat gac gca gta tcg atg cgc gtg tgg gaa cgc gga gtg 739 Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val Trp Glu Arg Gly Val 200 205 210						
ggc gaa acc cgc tcc tgt ggc acg gga acc gtt gct gca gcg tgt gct 787 Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val Ala Ala Ala Cys Ala 215 220 225						
gct tta gct gat gct gga ttg gga gaa ggc aca gct aaa gtg tgc gtt 835 Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr Ala Lys Val Cys Val						

230                      235                      240                      245

cca cgt ggg gaa gta gaa gtc cag atc ttt gac gac ggc tcc aca ctc    883  
 Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp Asp Gly Ser Thr Leu  
                          250                      255                      260

acc ggc cca agc gcc atc atc gca ctc ggt gag gtg cag atc                      925  
 Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu Val Gln Ile  
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taagattcgc gattgtagtt cgg                      948

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 <213> Corynebacterium glutamicum

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Ile Ile Pro Asp Glu Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val  
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Val Thr Leu Cys Asp Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu  
                           35                          40                          45

Arg Val Val Lys Ala Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser  
                           50                          55                          60

Leu Trp Phe Met Asp Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met  
   65                          70                          75                          80

Cys Gly Asn Gly Val Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly  
                           85                          90                          95

Leu Val Asp Asn Thr Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg  
                           100                          105                          110

His Val Asp Ile Leu Gln Ala Asp Gln His Ser Ala Gln Val Arg Val  
                           115                          120                          125

Asp Met Gly Ile Pro Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn  
                           130                          135                          140

Gly Gln Val Phe Ala Gly Leu Gly Val Asp Met Gly Asn Pro His Leu  
   145                          150                          155                          160

Ala Cys Val Val Pro Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu  
                           165                          170                          175

Leu Arg Ala Pro Thr Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn  
                           180                          185                          190

Val Glu Ile Val Thr Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val  
                           195                          200                          205

Trp Glu Arg Gly Val Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val  
   210                          215                          220

Ala Ala Ala Cys Ala Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr  
 225 230 235 240

Ala Lys Val Cys Val Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp  
 245 250 255

Asp Gly Ser Thr Leu Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu  
 260 265 270

Val Gln Ile  
 275

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ttatttaaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115  
 Leu Ala Leu Lys Gly  
 1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163  
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
 10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
 25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
 His Ser Trp Ser Ala Gln Asp Lys Ile Scr Pro Lys Val Trp Ala Ala  
 40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307  
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
 55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355  
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
 70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403  
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
 90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451  
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
 105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499  
 Ser M t Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
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gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly 135 140 145	547
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly 150 155 160 165	595
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr 170 175 180	643
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser 185 190 195	691
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys 200 205 210	739
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala 215 220 225	787
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro 230 235 240 245	835
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile 250 255 260	883
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys 265 270 275	931
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile 280 285 290	979
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile 295 300 305	1027
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser 310 315 320 325	1075
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys 330 335 340	1123
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala 345 350 355	1171
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu 360 365 370	1219

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca 1267  
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 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa 1315  
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
 390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac 1363  
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
 410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg 1411  
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
 425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg 1459  
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<211> 456

<212> PRT

<213> Corynebacterium glutamicum

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Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
 50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
 130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160



His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
 180 185 190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
 195 200 205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
 355 360 365  
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
 370 375 380  
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
 385 390 395 400  
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser  
 405 410 415  
 Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu  
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 Leu Thr Phe Ala Gly Ala Leu Phe  
 450 455

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&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1330)

&lt;223&gt; FRXA01009

&lt;400&gt; 11

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ttattttaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
                                         Leu Ala Leu Lys Gly
                                         1       5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
                        10                        15                        20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
                        25                        30                        35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
                        40                        45                        50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
                        55                        60                        65

atg ggt tcc caa ctt gtc tgc gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Phe His Asn Asn Pro Arg
                        70                        75                        80                        85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
                        90                        95                        100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
                        105                        110                        115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
                        120                        125                        130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
                        135                        140                        145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
                        150                        155                        160                        165

tcc gcg atg atg ctg acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
                        170                        175                        180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
                        185                        190                        195

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tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
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cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
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Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
375 380 385	
gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa	1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu	
390 395 400 405	
ttc aag gaa cgc ggc	1330
Phe Lys Glu Arg Gly	
410	

&lt;210&gt; 12

&lt;211&gt; 410

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 12

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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
 50 55 60  
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85 90 95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
 130 135 140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
 180 185 190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
 195 200 205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly

305		310		315		320
Ser Glu Ala Tyr	Ser Gly Gly Leu Thr	Tyr Ser Gly His Pro	Leu Ala			
	325	330	335			
Val Ala Pro Ala	Lys Ala Ala Leu Glu	Ile Tyr Ala Glu Gly	Glu Ile			
	340	345	350			
Ile Pro Arg Val	Ala Arg Leu Gly Ala	Glu Leu Ile Glu Pro	Arg Leu			
	355	360	365			
Arg Glu Leu Ala	Glu Glu Asn Val Ala	Ile Ala Asp Val	Arg Gly Ile			
	370	375	380			
Gly Phe Phe Trp	Ala Val Glu Phe Asn Ala	Asp Ala Thr Ala	Met Ala			
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Ala Gly Ala Ala	Glu Phe Lys Glu Arg	Gly				
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 <212> DNA  
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 Val Glu Trp Thr Ala  
 1 5  
 ttt ggc acc ctg att ctg ctc aat ttg gtg ggc agt tta tcc ccg ggg 163  
 Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly  
 10 15 20  
 cct gat acc ttt ttc ctc ctc cgc tta gcc acc cgc tcc aga gcg cac 211  
 Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His  
 25 30 35  
 gcg atc gct ggc gtc gcc ggc atc gtc acc gga ctc acg gtg tgg gtg 259  
 Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val  
 40 45 50  
 acg ctg acg gtc gtg gga gca gcg gcg ctg ctc acc act tat ccg tcg 307  
 Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu Thr Thr Tyr Pro Ser  
 55 60 65  
 att ctc gga atc atc cag ctc gtc ggc ggc acg tac cta agc ttc att 355  
 Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile  
 70 75 80 85  
 ggg tac aaq ttg ctg cgc tcg gcg tcg aga gag ctt atc gac gcc cgc 403  
 Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu Leu Ile Asp Ala Arg  
 90 95 100

cag ttc cgt ttc aac gcc gat gcc cga cct atc ccg gat gcg gta gaa 451  
 Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu  
 105 110 115  
 gca ctg gga acc cgc act cag gta tat cga caa ggt ttg gcc acc aac 499  
 Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn  
 120 125 130  
 ctg tca aac cct aaa gtt gtc atg tac ttc gcg gca att ctg gct ccg 547  
 Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro  
 135 140 145  
 ttg atg cca gcg cac cca tca ccg gtg ctg gcg ttc tct atc atc gtg 595  
 Leu Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val  
 150 155 160 165  
 gcg att tta gtg cag acc ttt gtt acc ttc tct gct gtg tgc ctc att 643  
 Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile  
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 Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp  
 185 190 195  
 ttt gac ctg ctt gct ggc gtt gtc ttc ctc gtt gtg ggt gtg act ctg 739  
 Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu  
 200 205 210  
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 tcc 792

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 Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly  
 35 40 45  
 Leu Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu  
 50 55 60  
 Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr  
 65 70 75 80  
 Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu  
 85 90 95  
 Leu Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile

100	105	110
Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln 115 120 125		
Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala 130 135 140		
Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala 145 150 155 160		
Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser 165 170 175		
Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu 180 185 190		
Arg Ala Gly Pro Trp Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val 195 200 205		
Val Gly Val Thr Leu Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly 210 215 220		

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 <213> Corynebacterium glutamicum

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	Leu Leu Leu Gly Gly	
	1 5	
aac cct gcc gag atc gac cag gtt tta ggt ggc gat caa acc cag atc		163
Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile		
10 15 20		
gag tct gga gag tcc acc gga gcc ggc gac ttt gat cac tgc caa acc		211
Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr		
25 30 35		
ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tac acc tca		259
Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Tyr Thr Ser		
40 45 50		
ttc tcc gtc aat gaa atg tgg cag act ttg ctt cca gct cag gct ggt		307
Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly		
55 60 65		
atc gaa tac acc gag ccg aca ttg act ctt ttc aaa aac tcc acc caa		355
Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln		
70 75 80 85		

acc ggc tgc ggt ttc gct tct gcg tcc act ggg ccg ttt tac tgt ccg 403  
 Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro  
 90 95 100

tca gac caa gat gct tat ttt gac ttg act ttc ttc gat cag atg cgt 451  
 Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg  
 105 110 115

cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg tac atc gtg gcg 499  
 Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala  
 120 125 130

cac gag tac ggc cac cac gtc caa aac ctc gag ggc aca ctc gga ctg 547  
 His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu  
 135 140 145

tcc aat tac aac gat ccg ggc gct gat tcc aac gcc gtc aag atc gag 595  
 Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu  
 150 155 160 165

ttg cag gcc gat tgc tac gca ggc att tgg gct aat cac tcc agc gaa 643  
 Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu  
 170 175 180

ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct gag cta gat tcc 691  
 Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser  
 185 190 195

gct ctc ctc gct gca agc gcc gtg ggc gac gac aat atc cag caa cga 739  
 Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn Ile Gln Gln Arg  
 200 205 210

tcc ggt ggc gat gtc aat cct gaa agc tgg act cac ggc tca tcg cag 787  
 Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln  
 215 220 225

cag cgc aaa gac gcg ttc ctc gcc ggc tac aac acc ggc cag atg agc 835  
 Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser  
 230 235 240 245

gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac gct taaagcattg 884  
 Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp Ala  
 250 255

cttttcgacg tct 897

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 <212> PRT  
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Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg  
 35 40 45



Leu Tyr Tyr Thr Ser Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu  
 50 55 60  
 Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe  
 65 70 75 80  
 Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly  
 85 90 95  
 Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe  
 100 105 110  
 Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln  
 115 120 125  
 Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu  
 130 135 140  
 Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn  
 145 150 155 160  
 Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala  
 165 170 175  
 Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu  
 180 185 190  
 Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp  
 195 200 205  
 Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr  
 210 215 220  
 His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn  
 225 230 235 240  
 Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn  
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 Asp Ala

<210> 17  
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 Val Ser Arg Ile Tyr  
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gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
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gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
Asp Ala Val Lys Ala Gly Gln Leu Val Leu Pro Thr Asp Thr Leu
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tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
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ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
      55                      60                      65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
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gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
      90                      95                      100

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc 451
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
      105                      110                      115

acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
      120                      125                      130

cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
      135                      140                      145

act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595
Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
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gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643
Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
      170                      175                      180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691
Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
      185                      190                      195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa 739
Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
      200                      205                      210

agc ctg cgc taaatgggag tcggtttcgc ggg 771
Ser Leu Arg
      215

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&lt;210&gt; 18

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 18

Val Ser Arg Ile Tyr Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly  
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Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu  
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Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu  
 35 40 45

Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro  
 50 55 60

Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His  
 65 70 75 80

Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly  
 85 90 95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu  
 100 105 110

Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val  
 115 120 125

Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala  
 130 135 140

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln  
 145 150 155 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala  
 165 170 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys  
 180 185 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu  
 195 200 205

Gly Val Ser Ala Glu Ser Leu Arg  
 210 215

&lt;210&gt; 19

&lt;211&gt; 1026

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1003)

&lt;223&gt; RXC00657

&lt;400&gt; 19

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tgtaacgcag gattcaccaa tcaatgaaag gtcgaccgac atg agc act gaa gac 115  
 Met Ser Thr Glu Asp  
 1 5

att gtc gtc gta gca gta gat ggc tgc gac gcc tca aaa caa gct gtt	163
Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val	
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cggtgg gct gca aat acc gcc aac aaa cgt ggc att cca ctt cgc ttg	211
Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu	
25 30 35	
gct tcc agc tac acc atg cct cag ttc ctc tac gca gag gga atg gtt	259
Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val	
40 45 50	
cca cca caa gag ctt ttc gat gac ctc cag gcc gaa gcc ctg gaa aag	307
Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys	
55 60 65	
att aac gaa gcc cgt gac atc gcc cat gag gta gcg cca gaa atc aag	355
Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys	
70 75 80 85	
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Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu	
90 95 100	
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Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly	
105 110 115	
gga ctc tcc gga atg gtc atg ggc tcc gtc tcc ggt gca gtg gtc agc	499
Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser	
120 125 130	
cac gca aag tgt cca gtc gtt gtt gtc cgt gaa gac agc gca gtc aac	547
His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn	
135 140 145	
gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa	595
Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu	
150 155 160 165	
gtc tcc caa cag gca acc gaa tac gca ttt gcg gaa gct gaa gct cgt	643
Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg	
170 175 180	
ggc gcc gaa ctc gtt gca gtt cac acc tgg atg gac atg cag gta cag	691
Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln	
185 190 195	
gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg	739
Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln Gln Trp Asp Glu Val	
200 205 210	
gaa cgt cag caa acc gac atg ctg atc gaa cgc ctc gca cca ctg gtg	787
Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val	
215 220 225	
gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac cgc	835
Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg	
230 235 240 245	

cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc 883  
 Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val  
                   250                  255                  260

gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc 931  
 Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser  
                   265                  270                  275

acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt 979  
 Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val  
                   280                  285                  290

cgc cca cct gag aag att aag aag tagttttcttt taagtttcga tgc 1026  
 Arg Pro Pro Glu Lys Ile Lys Lys  
                   295                  300

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 <212> PRT  
 <213> Corynebacterium glutamicum

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Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly  
                   20                  25                  30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr  
                   35                  40                  45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala  
                   50                  55                  60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val  
                   65                  70                  75                  80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile  
                   85                  90                  95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly  
                   100                  105                  110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser  
                   115                  120                  125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu  
                   130                  135                  140

Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly  
                   145                  150                  155                  160

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala  
                   165                  170                  175

Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met  
                   180                  185                  190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln  
                   195                  200                  205

Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg  
 210 215 220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile  
 225 230 235 240

Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn  
 245 250 255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly  
 260 265 270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys  
 275 280 285

Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys  
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 <223> RXC00552

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 Val Ala Thr Ser Lys  
 1 5

att ctt ctt tat tac gca ttc acc ccg ctc tct gac cct aaa gcg gtt 163  
 Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val  
 10 15 20

cag ctg tgg cag cgt gag ctc tgc gag tca ctg aat ctt cgt ggc cgc 211  
 Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu Asn Leu Arg Gly Arg  
 25 30 35

atc ctg atc tcc act cac ggc atc aat gga acc gtg ggc gga gat att 259  
 Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr Val Gly Gly Asp Ile  
 40 45 50

gat gat tgc aag gcg tac att aaa aag acc cgc gag tac cca ggt ttc 307  
 Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg Glu Tyr Pro Gly Phe  
 55 60 65

aac cgc atg cag ttt aag tgg tcc gag ggt ggc gct gag gat ttc cca 355  
 Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro  
 70 75 80 85

aag ctc agt gtc aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca 403  
 Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro  
 90 95 100

gat gag ctc aaa gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac 451  
Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val Gly Gly Val His  
105 110 115

ctg aaa cca cag cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa 499  
Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu  
120 125 130

gtt gtg ttc ttt gac ggc cgc aac gca atg gaa gcc cag atc ggc aag 547  
Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys  
135 140 145

ttc aag gac gct gtt gtc cct gac gta gaa acc act cat gat ttc atc 595  
Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile  
150 155 160 165

gca gaa att gag tct gga aaa tac gac gat ctc aaa gac aag cct gtg 643  
Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val  
170 175 180

gtc acc tac tgc acc ggc gga att cgt tgt gag atc ctg agt tca ctc 691  
Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu  
185 190 195

atg atc aac cgt ggt ttc aaa gag gtc tac caa atc gat ggc ggc atc 739  
Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile  
200 205 210

gtt cgc tac ggc gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc 787  
Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser  
215 220 225

ctc tac gtt ttc gat aag cgc atg cat atg gaa ttc ggc gag gat tac 835  
Leu Tyr Val Phe Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr  
230 235 240 245

aaa gag gtc gga cac tgc atc cat tgc gat act ccc acc aac aaa ttt 883  
Lys Glu Val Gly His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe  
250 255 260

gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc 931  
Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys  
265 270 275

cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc 979  
Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg  
280 285 290

tgt gca gca att gct gcg gat ttc gct gag caa gga att gat ccg ctc 1027  
Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu  
295 300 305

gtt act tct taaaaagggt atgggtggctg ggt 1059  
Val Thr Ser  
310

&lt;210&gt; 22

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 22

Val Ala Thr Ser Lys Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser  
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 Asp Pro Lys Ala Val Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu  
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 Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr  
 35 40 45  
 Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg  
 50 55 60  
 Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly  
 65 70 75 80  
 Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val  
 85 90 95  
 Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val  
 100 105 110  
 Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu  
 115 120 125  
 Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu  
 130 135 140  
 Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr  
 145 150 155 160  
 Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu  
 165 170 175  
 Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu  
 180 185 190  
 Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln  
 195 200 205  
 Ile Asp Gly Gly Ile Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly  
 210 215 220  
 Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu  
 225 230 235 240  
 Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr  
 245 250 255  
 Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu  
 260 265 270  
 Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His  
 275 280 285  
 Cys Lys Arg Glu Arg Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln  
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 Gly Ile Asp Pro Leu Val Thr Ser  
 305 310



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<210> 23
<211> 1386
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101)..(1363)  
<223> RXP.00534
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											gtg	gcc	ctg	gtc	gta	
											Val	Ala	Leu	Val	Val	
											1				5	
cag aaa tat ggc ggt tcc tcg ctt gag agt gcg gaa cgc att aga aac																163
Gln	Lys	Tyr	Gly	Gly	Ser	Ser	Leu	Glu	Ser	Ala	Glu	Arg	Ile	Arg	Asn	
				10					15					20		
gtc gct caa cgg atc gtt gcc acc aag aag gct gga aat gat gtc gtg																211
Val	Ala	Glu	Arg	Ile	Val	Ala	Thr	Lys	Lys	Ala	Gly	Asn	Asp	Val	Val	
			25					30					35			
gtt gtc tgc tcc gca atg gga gac acc acg gat gaa ctt cta gaa ctt																259
Val	Val		Ser	Ala	Met	Gly	Asp	Thr	Thr	Asp	Glu	Leu	Leu	Glu	Leu	
		40					45					50				
gca ccg gca gtg aat ccc gtt ccg cca gct cgt gaa atg gat atg ctc																307
Ala	Ala	Ala	Val	Asn	Pro	Val	Pro	Pro	Ala	Arg	Glu	Met	Asp	Met	Leu	
		55				60					65					
ctg act gct ggt gag cgt att tct aac gct ctc gtc gcc atg gct att																355
Leu	Thr	Ala	Gly	Glu	Arg	Ile	Ser	Asn	Ala	Leu	Val	Ala	Met	Ala	Ile	
	70				75					80				85		
gag tcc ctt ggc gca gaa gcc caa tct ttc acg ggc tct cag gct ggt																403
Glu	Ser	Leu	Gly	Ala	Glu	Ala	Gln	Ser		Phe	Thr	Gly	Ser	Gln	Ala	Gly
				90					95					100		
glg ctc acc acc gag cgc cac gga aac gca cgc att gtt gat gtc act																451
Val	Leu	Thr		Glu	Arg	His	Gly	Asn	Ala	Arg	Ile	Val	Asp	Val	Thr	
			105					110					115			
cca cgt cgt gtg cgt gaa gca ctc gat gag ggc aag atc tgc att gtt																499
Pro	Gly	Arg	Val	Arg	Glu	Ala	Leu	Asp	Glu	Gly	Lys	Ile	Cys	Ile	Val	
		120					125					130				
gcl cgt ttc cag ggt gtt aat aaa gaa acc cgc gat gtc acc acg ttg																547
Ala	Gly	Phe	Gln	Gly	Val	Asn	Lys	Glu	Thr	Arg	Asp	Val	Thr	Thr	Leu	
	135					140					145					
ggt cgt ggt ggt tct gac acc act gca gtt gcg ttg gca gct gct ttg																595
Gly	Arg	Gly	Gly	Ser	Asp	Thr	Thr	Ala	Val	Ala	Leu	Ala	Ala	Ala	Leu	
	150				155					160					165	
aac gct gat gtg tgt gag att tac tcg gac gtt gac ggt gtg tat acc																643
Asn	Ala	Asp	Val	Cys	Glu	Ile	Tyr	Ser	Asp	Val	Asp	Gly	Val	Tyr	Thr	

170										175										180									
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Ala	Asp	Pro	Arg	Ile	Val	Pro	Asn	Ala	Gln	Lys	Leu	Glu	Lys	Leu	Ser	691													
			185					190					195																
ttc	gaa	gaa	atg	ctg	gaa	ctt	gct	gct	gtt	ggc	tcc	aag	att	ttg	gtg	739													
Phe	Glu	Glu	Met	Leu	Glu	Leu	Ala	Ala	Val	Gly	Ser	Lys	Ile	Leu	Val														
		200					205					210																	
ctg	cgc	agt	gtt	gaa	tac	gct	cgt	gca	ttc	aat	gtg	cca	ctt	cgc	gta	787													
Leu	Arg	Ser	Val	Glu	Tyr		Arg	Ala	Phe	Asn	Val	Pro	Leu	Arg	Val														
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cgc	tcg	tct	tat	agt	aat	gat	ccc	ggc	act	ttg	att	gcc	ggc	tct	atg	835													
Arg	Ser	Ser	Tyr	Ser	Asn	Asp	Pro	Gly	Thr	Leu	Ile	Ala	Gly	Ser	Met														
230					235					240					245														
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Glu	Asp	Ile	Pro	Val	Glu	Glu	Ala	Val	Leu	Thr	Gly	Val	Ala	Thr	Asp														
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Lys	Ser	Glu	Ala	Lys	Val	Thr	Val	Leu	Gly	Ile	Ser	Asp	Lys	Pro	Gly														
			265					270					275																
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Glu	Ala	Ala	Lys	Val	Phe	Arg	Ala	Leu	Ala	Asp	Ala	Glu	Ile	Asn	Ile														
		280					285					290																	
gac	atg	gtt	ctg	cag	aac	gtc	tct	tct	gta	gaa	gac	ggc	acc	acc	gac	1027													
Asp	Met	Val	Leu	Gln	Asn	Val	Ser	Ser	Val	Glu	Asp	Gly	Thr	Thr	Asp														
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atc	acc	ttc	acc	tgc	cct	cgt	tcc	gac	ggc	cgc	cgc	gcg	atg	gag	atc	1075													
Ile	Thr	Phe	Thr	Cys	Pro	Arg	Ser	Asp	Gly	Arg	Arg	Ala	Met	Glu	Ile														
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Asp	Gln	Val	Gly	Lys	Val	Ser	Leu	Val	Gly	Ala	Gly	Met	Lys	Ser	His														
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cca	ggg	gtt	acc	gca	gag	ttc	atg	gaa	gct	ctg	cgc	gat	gtc	aac	gtg	1219													
Pro	Gly	Val	Thr	Ala	Glu	Phe	Met	Glu	Ala	Leu	Arg	Asp	Val	Asn	Val														
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aac	atc	gaa	ttg	att	tcc	acc	tct	gag	att	cgt	att	tcc	gtg	ctg	atc	1267													
Asn	Ile	Glu	Leu	Ile	Ser	Thr	Ser	Glu	Ile	Arg	Ile	Ser	Val	Leu	Ile														
		375				380					385																		
cgt	gaa	gat	gat	ctg	gat	gct	gct	gca	cgt	gca	ttg	cat	gag	cag	ttc	1315													
Arg	Glu	Asp	Asp	Leu	Asp	Ala	Ala	Ala	Arg	Ala	Leu	His	Glu	Gln	Phe														
390					395				400					405															
cag	ctg	ggc	ggc	gaa	gac	gaa	gcc	gtc	gtt	tat	gca	ggc	acc	gga	cgc	1363													
Gln	Leu	Gly	Gly	Glu	Asp	Glu	Ala	Val	Val	Tyr	Ala	Gly	Thr	Gly	Arg														
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1386

&lt;210&gt; 24

&lt;211&gt; 421

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 24

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Glu	Arg	Ile	Arg	Asn	Val	Ala	Glu	Arg	Ile	Val	Ala	Thr	Lys	Lys	Ala
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Gly	Asn	Asp	Val	Val	Val	Val	Cys	Ser	Ala	Met	Gly	Asp	Thr	Thr	Asp
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Glu	Leu	Leu	Glu	Leu	Ala	Ala	Ala	Val	Asn	Pro	Val	Pro	Pro	Ala	Arg
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Glu	Met	Asp	Met	Leu	Leu	Thr	Ala	Gly	Glu	Arg	Ile	Ser	Asn	Ala	Leu
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Val	Ala	Met	Ala	Ile	Glu	Ser	Leu	Gly	Ala	Glu	Ala	Gln	Ser	Phe	Thr
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Gly	Ser	Gln	Ala	Gly	Val	Leu	Thr	Thr	Glu	Arg	His	Gly	Asn	Ala	Arg
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Ile	Val	Asp	Val	Thr	Pro	Gly	Arg	Val	Arg	Glu	Ala	Leu	Asp	Glu	Gly
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Lys	Ile	Cys	Ile	Val	Ala	Gly	Phe	Gln	Gly	Val	Asn	Lys	Glu	Thr	Arg
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Asp	Val	Thr	Thr	Leu	Gly	Arg	Gly	Gly	Ser	Asp	Thr	Thr	Ala	Val	Ala
	145				150					155					160

Leu	Ala	Ala	Ala	Leu	Asn	Ala	Asp	Val	Cys	Glu	Ile	Tyr	Ser	Asp	Val
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Asp	Gly	Val	Tyr	Thr	Ala	Asp	Pro	Arg	Ile	Val	Pro	Asn	Ala	Gln	Lys
		180						185					190		

Leu	Glu	Lys	Leu	Ser	Phe	Glu	Glu	Met	Leu	Glu	Leu	Ala	Ala	Val	Gly
		195					200					205			

Ser	Lys	Ile	Leu	Val	Leu	Arg	Ser	Val	Glu	Tyr	Ala	Arg	Ala	Phe	Asn
	210					215					220				

Val	Pro	Leu	Arg	Val	Arg	Ser	Ser	Tyr	Ser	Asn	Asp	Pro	Gly	Thr	Leu
	225				230					235					240

Ile	Ala	Gly	Ser	Met	Glu	Asp	Ile	Pro	Val	Glu	Glu	Ala	Val	Leu	Thr
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Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala L u Ala Asp  
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Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
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Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg  
 305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
 325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala  
 340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
 355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg  
 370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
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Ala Gly Thr Gly Arg  
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 Met Thr Thr Ile Ala  
 1 5

gtt gtt cgt gca acc ggc cag gtc ggc cag gtt atg cgc acc ctt ttg 163  
 Val Val Gly Ala Thr Gly Gln Val Gly Gln Val Met Arg Thr Leu Leu  
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gaa gag cgc aat ttc cca gct gac act gtt cgt ttc ttt gct tcc cca 211  
 Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg Phe Phe Ala Ser Pro  
 25 30 35

cgt tcc cca ggc cgt aag att gaa ttc cgt ggc acg gaa atc gag gta 259  
 Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly Thr Glu Ile Glu Val  
 40 45 50

gaa gac att act cag gca acc gag gag tcc ctc aag gac atc gac gtt 307

Glu	Asp	Ile	Thr	Gln	Ala	Thr	Glu	Glu	Ser	Leu	Lys	Asp	Ile	Asp	Val	
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Ala	Leu	Phe	Ser	Ala	Gly	Gly	Thr	Ala	Ser	Lys	Gln	Tyr	Ala	Pro	Leu	
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ttc	gct	gct	gca	ggc	gcg	act	gtt	gtg	gat	aac	tct	tct	gct	tgg	cgc	403
Phe	Ala	Ala	Ala	Gly	Ala	Thr	Val	Val	Asp	Asn	Ser	Ser	Ala	Trp	Arg	
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aag	gac	gac	gag	gtt	cca	cta	atc	gtc	tct	gag	gtg	aac	cct	tcc	gac	451
Lys	Asp	Asp	Ser	Glu	Val	Pro	Leu	Ile	Val	Ser	Glu	Val	Asn	Pro	Ser	Asp
			105					110					115			
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Lys	Asp	Ser	Leu	Val	Lys	Gly	Ile	Ile	Ala	Asn	Pro	Asn	Cys	Thr	Thr	
		120				125						130				
atg	gct	gcg	atg	cca	gtg	ctg	aag	cca	ctt	cac	gat	gcc	gct	ggt	ctt	547
Met	Ala	Ala	Met	Pro	Val	Leu	Lys	Pro	Leu	His	Asp	Ala	Ala	Gly	Leu	
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gta	aag	ctt	cac	gtt	tcc	tct	tac	cag	gct	gtt	tcc	ggt	tct	ggt	ctt	595
Val	Lys	Leu	His	Val	Ser	Ser	Tyr	Gln	Ala	Val	Ser	Gly	Ser	Gly	Leu	
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Ala	Gly	Val	Glu	Thr	Leu	Ala	Lys	Gln	Val	Ala	Ala	Val	Gly	Asp	His	
				170				175						180		
aac	gtt	gag	ttc	gtc	cat	gat	gga	cag	gct	gct	gac	gca	ggc	gat	gtc	691
Asn	Val	Glu	Phe	Val	His	Asp	Gly	Gln	Ala	Ala	Asp	Ala	Gly	Asp	Val	
			185					190					195			
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Gly	Pro	Tyr	Val	Ser	Pro	Ile	Ala	Tyr	Asn	Val	Leu	Pro	Phe	Ala	Gly	
		200				205						210				
aac	ctc	gtc	gat	gac	ggc	acc	ttc	gaa	acc	gat	gaa	gag	cag	aag	ctg	787
Asn	Leu	Val	Asp	Asp	Gly	Thr	Phe	Glu	Thr	Asp	Glu	Glu	Gln	Lys	Leu	
	215					220					225					
cgc	aac	gaa	tcc	cgc	aag	att	ctc	ggt	ctc	cca	gac	ctc	aag	gtc	tca	835
Arg	Asn	Glu	Ser	Arg	Lys	Ile	Leu	Gly	Leu	Pro	Asp	Leu	Lys	Val	Ser	
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ggc	acc	tgc	gtc	cgc	gtg	ccg	gtt	ttc	acc	ggc	cac	acg	ctg	acc	att	883
Gly	Thr	Cys	Val	Arg	Val	Pro	Val	Phe	Thr	Gly	His	Thr	Leu	Thr	Ile	
			250					255						260		
cac	gcc	gaa	ttc	gac	aag	gca	atc	acc	gtg	gac	cag	gcg	cag	gag	atc	931
His	Ala	Glu	Phe	Asp	Lys	Ala	Ile	Thr	Val	Asp	Gln	Ala	Gln	Glu	Ile	
			265				270						275			
ttg	ggt	gcc	gct	tca	ggc	gtc	aag	ctt	gtc	gac	gtc	cca	acc	cca	ctt	979
Leu	Gly	Ala	Ala	Ser	Gly	Val	Lys	Leu	Val	Asp	Val	Pro	Thr	Pro	Leu	
		280				285						290				
gca	gct	gcc	ggc	att	gac	gaa	tcc	ctc	gtt	gga	cgc	atc	cgt	cag	gac	1027
Ala	Ala	Ala	Gly	Ile	Asp	Glu	Ser	L u	Val	Gly	Arg	Ile	Arg	Gln	Asp	

295                      300                      305  
 tcc act gtc gac gat aac cgc ggt ctg gtt ctc gtc gta tct ggc gac 1075  
 Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu Val Val Ser Gly Asp  
 310                      315                      320                      325  
 aac ctc cgc aag ggt gct gcg cta aac acc atc cag atc gct gag ctg 1123  
 Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile Gln Ile Ala Glu Leu  
 330                      335                      340  
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 Leu Val Lys

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 Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly  
 35                      40                      45  
 Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu  
 50                      55                      60  
 Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys  
 65                      70                      75                      80  
 Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn  
 85                      90                      95  
 Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu  
 100                      105                      110  
 Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn  
 115                      120                      125  
 Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His  
 130                      135                      140  
 Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val  
 145                      150                      155                      160  
 Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala  
 165                      170                      175  
 Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala  
 180                      185                      190  
 Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val  
 195                      200                      205  
 Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp

210	215	220
Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro		
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Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly		
	245	250 255
His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp		
	260	265 270
Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp		
	275	280 285
Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly		
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Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu		
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Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile		
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Gln Ile Ala Glu Leu Leu Val Lys		
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 Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser  
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 acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158  
 Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp  
 15 20 25 30  
 cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206  
 Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val  
 35 40 45  
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 Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr  
 50 55 60  
 gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt 302  
 Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val  
 65 70 75  
 ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac 350

Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn  
 80 85 90  
 aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca 398  
 Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala 110  
 95 100 105  
 ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc 446  
 Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser 125  
 115 120  
 gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg 494  
 Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val 140  
 130 135  
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 Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp 155  
 145 150  
 ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590  
 Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr 170  
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 ctc ggc gct tcc atg gtt 608  
 Leu Gly Ala Ser Met Val  
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 Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr  
 50 55 60  
 Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg  
 65 70 75 80  
 Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val  
 85 90 95  
 Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr  
 100 105 110  
 Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp  
 115 120 125  
 Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile  
 130 135 140



Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr  
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Ala Ser Met Val  
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Val Asn Ser Glu Leu  
1 5

aaa cca gga tta gat ctc ctc ggc gac cca att gtc ctt act caa cgt 163  
Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile Val Leu Thr Gln Arg  
10 15 20

ttg gta gat ata ccg agt ccg tcc ggt cag gaa aag cag att gct gat 211  
Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu Lys Gln Ile Ala Asp  
25 30 35

gaa att gaa gat gcc ctt cgg aac ctt aat cta cct ggt gta gag gtc 259  
Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val  
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ttc cgc ttc aac aac aac gtt ctt gct cgc acg aac agg gga ttg gcc 307  
Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr Asn Arg Gly Leu Ala  
55 60 65

tcg agg gtc atg ctt gct ggt cat atc gat aca gtg ccg atc gcg gac 355  
Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp  
70 75 80 85

aat ctg cca agc cgt gtg gaa gac ggc atc atg tat ggc tgt ggc acc 403  
Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr  
90 95 100

gtc gat atg aaa tct ggg ttg gcg gtg tat ttg cat act ttt gcc acc 451  
Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr  
105 110 115

ttg gcc acg tcg act gag ctt aaa cat gat ctg acg ctg att gcg tat 499  
Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu Thr Leu Ile Ala Tyr  
120 125 130

gag tgc gag gaa gtt gct gat cac ctc aat ggt ttg ggc cac att cgc 547  
Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly Leu Gly His Ile Arg

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aag gtg acg gcg cat ggt gtg cgt gcc cat tcg gcg aga agc tgg ttg Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu 185 190 195			691
ggt gat aat gcg atg cat aag ttg tcg ccg atc att tcg aag gtt gct Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala 200 205 210			739
gcg tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu 215 220 225			787
ggc ctc aac atc gtt ttc tgc gaa tcg ggc gtg gca aac aac gtc att Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile 230 235 240 245			835
cca gac ctc gcg tgg atg aac ctc aac ttc cgt ttc gcg ccg aat cgc Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg 250 255 260			883
gat ctc aac gag gcg atc gag cat gtc gtc gaa acg ctt gag ctt gac Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp 265 270 275			931
ggt caa gac ggc atc gaa tgg gcc gta gaa gac ggg gca ggc ggt gcc Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala 280 285 290			979
ctt cca ggc ttg ggg cag cag gtg aca agc ggg ctt atc gac gcc gtc Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val 295 300 305			1027
ggc cgc gaa aaa atc cgc gca aaa ttc ggc tgg acc gat gtc tca cgt Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp Thr Asp Val Ser Arg 310 315 320 325			1075
ttt tca gcc atg gga att cca gcc cta aac ttt ggc gct ggt gat cca Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe Gly Ala Gly Asp Pro 330 335 340			1123
agt ttc gcg cat aaa cgc gac gag cag tgc cca gtg gag caa atc acg Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro Val Glu Gln Ile Thr 345 350 355			1171
gat gtg gca gca att ttg aag cag tac ctg agc gag taaccgcatt Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser Glu 360 365			1217
cggggttatc gtg			1230

&lt;210&gt; 30

&lt;211&gt; 369

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 30

Val Asn Ser Glu Leu Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile  
 1 5 10 15

Val Leu Thr Gln Arg Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu  
 20 25 30

Lys Gln Ile Ala Asp Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu  
 35 40 45

Pro Gly Val Glu Val Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr  
 50 55 60

Asn Arg Gly Leu Ala Ser Arg Val Met Leu Ala Gly His Ile Asp Thr  
 65 70 75 80

Val Pro Ile Ala Asp Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met  
 85 90 95

Tyr Gly Cys Gly Thr Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu  
 100 105 110

His Thr Phe Ala Thr Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu  
 115 120 125

Thr Leu Ile Ala Tyr Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly  
 130 135 140

Leu Gly His Ile Arg Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu  
 145 150 155 160

Ala Leu Leu Gly Glu Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln  
 165 170 175

Gly Asn Leu Arg Ile Lys Val Thr Ala His Gly Val Arg Ala His Ser  
 180 185 190

Ala Arg Ser Trp Leu Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile  
 195 200 205

Ile Ser Lys Val Ala Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly  
 210 215 220

Leu Thr Tyr Arg Glu Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val  
 225 230 235 240

Ala Asn Asn Val Ile Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg  
 245 250 255

Phe Ala Pro Asn Arg Asp Leu Asn Glu Ala Ile Glu His Val Val Glu  
 260 265 270

Thr Leu Glu Leu Asp Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp  
 275 280 285

Gly Ala Gly Gly Ala Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly

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ttctcaccgc cactcgttcc ctcaaccac aaggagcacc																	
												atg	gct	tcc	gca	act	115
												Met	Ala	Ser	Ala	Thr	
												1				5	
ttc acc ggc gtg atc cca ccc gta atg acc cca ctc cac gcc gac ggc																	163
Phe	Thr	Gly	Val	Ile	Pro	Pro	Val	Met	Thr	Pro	Leu	His	Ala	Asp	Gly		
				10					15					20			
agt gtg gat gta gaa agc ctc cgc aag ctc gtt gac cac ctc atc aat																	211
Ser	Val	Asp	Val	Glu	Ser	Leu	Arg	Lys	Leu	Val	Asp	His	Leu	Ile	Asn		
				25					30					35			
ggg ggc gtc gac gga ctt ttc gca ctg ggc tcc tca ggc gaa gcg gca																	259
Gly	Gly	Val	Asp	Gly	Leu	Phe	Ala	Leu	Gly	Ser	Ser	Gly	Glu	Ala	Ala		
				40					45					50			
ttc ctc acc cgc gcc cag cgc aaa ctc gca ctg acc acc atc atc gag																	307
Phe	Leu	Thr	Arg	Ala	Gln	Arg	Lys	Leu	Ala	Leu	Thr	Thr	Ile	Ile	Glu		
				55					60					65			
cac acc gca ggc cgc gtt ccc gta act gct ggt gtc att gaa acc acc																	355
His	Thr	Ala	Gly	Arg	Val	Pro	Val	Thr	Ala	Gly	Val	Ile	Glu	Thr	Thr		
				70					75					80	85		
act gct cgc gtg att qag ctc qtg qaa gat gcc ctg gag gct ggt gcc																	403
Thr	Ala	Arg	Val	Ile	Glu	Leu	Val	Glu	Asp	Ala	Leu	Glu	Ala	Gly	Ala		
				90					95					100			
gaa ggc ctc gtt gcc acc gca cct ttc tac acc cgc acc cac gat gtg																	451
Glu	Gly	Leu	Val	Ala	Thr	Ala	Pro	Phe	Tyr	Thr	Arg	Thr	His	Asp	Val		

105	110	115	
gaa att gaa gaa cac ttc cgc aag atc cac gcc gcc gct cca gag ctt Glu Ile Glu Glu His Phe Arg Lys Ile His Ala Ala Ala Pro Glu Leu 120 125 130			499
cca ctg ttt gcc tac aac atc cca gtg tgg gtg cac tcc aac ctc aac Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val His Ser Asn Leu Asn 135 140 145			547
cca gtc atg ctt ttg acg ctg gcc aag gat ggc gtt ctt gca ggc acc Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly Val Leu Ala Gly Thr 150 155 160 165			595
aag gat tcc agt ggc aat gat ggc gca atc cgc tca ctg atc gaa gct Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg Ser Leu Ile Glu Ala 170 175 180			643
cgt gat gat gct gga ctc act gag cag ttc aag atc ctc acc ggc agc Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys Ile Leu Thr Gly Ser 185 190 195			691
gaa acc acc gtc gat ttc gcc tac ctt ggc ggt gcc gat gga gtt gtc Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly Ala Asp Gly Val Val 200 205 210			739
cca ggc ctg ggc aat gtt gat cct gca gca tac gca gct tta gca aaa Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr Ala Ala Leu Ala Lys 215 220 225			787
ctc tgc ctc gat gga aag tgg gca gaa gct gct gct ttg cag aag cgc Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala Ala Leu Gln Lys Arg 230 235 240 245			835
atc aac cac ctc ttc cac atc gtc ttc gtg gga gac acc tcc cat atg Ile Asn His Leu Phe His Ile Val Phe Val Gly Asp Thr Ser His Met 250 255 260			883
tcc gga tcc agc gct ggt ttg ggc ggt ttc aag aca gca ctc gca cac Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His 265 270 275			931
ctt ggc att att gaa tcc aat gcg atg gca gtt cct cac cag agc ctc Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu 280 285 290			979
agc gac gaa gaa act gct cgc att cac gcc att gtt gat gaa ttc ctg Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu 295 300 305			1027
tac acc gct taaggccac acctcatgac tga Tyr Thr Ala 310			1059

&lt;210&gt; 32

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 32

Met Ala Ser Ala Thr Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro  
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 Leu His Ala Asp Gly Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val  
 20 25 30  
 Asp His Leu Ile Asn Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser  
 35 40 45  
 Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu  
 50 55 60  
 Thr Thr Ile Ile Glu His Thr Ala Gly Arg Val Pro Val Thr Ala Gly  
 65 70 75 80  
 Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala  
 85 90 95  
 Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr  
 100 105 110  
 Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala  
 115 120 125  
 Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val  
 130 135 140  
 His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly  
 145 150 155 160  
 Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg  
 165 170 175  
 Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys  
 180 185 190  
 Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly  
 195 200 205  
 Ala Asp Gly Val Val Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr  
 210 215 220  
 Ala Ala Leu Ala Lys Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala  
 225 230 235 240  
 Ala Leu Gln Lys Arg Ile Asn His Leu Phe His Ile Val Phe Val Gly  
 245 250 255  
 Asp Thr Ser His Met Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys  
 260 265 270  
 Thr Ala Leu Ala His Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val  
 275 280 285  
 Pro His Gln Ser Leu Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile  
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 Val Asp Glu Phe Leu Tyr Thr Ala  
 305 310

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<223> RXA00863
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Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln Thr Ile Val Ala Ala  
10 15 20

gtc aat gag tcc gac gat ctg gag ctt gtt gca gag atc ggc gtc gac 211  
Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala Glu Ile Gly Val Asp  
25 30 35

gat gat ttg agc ctt ctg gta gac aac ggc gct gaa gtt gtc gtt gac 259  
Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala Glu Val Val Val Asp  
40 45 50

ttc acc act cct aac gct gtg atg ggc aac ctg gag ttc tgc atc aac 307  
Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu Glu Phe Cys Ile Asn  
55 60 65

aac ggc att tct gcg gtt gtt gga acc acg ggc ttc gat gat gct cgt 355  
Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly Phe Asp Asp Ala Arg  
70 75 80 85

ttg gag cag gtt cgc gac tgg ctt gaa gga aaa gac aat gtc ggt gtt 403  
Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys Asp Asn Val Gly Val  
90 95 100

ctg atc gca cct aac ttt gct atc tct gcg gtg ttg acc atg gtc ttt 451  
Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val Leu Thr Met Val Phe  
105 110 115

tcc aag cag gct gcc cgc ttc ttc gaa tca gct gaa gtt att gag ctg 499  
Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala Glu Val Ile Glu Leu  
120 125 130

cac cac ccc aac aag ctg gat gca cct tca ggc acc gcg atc cac act 547  
 His His Pro Asn Lys Leu Asp Ala Pro Ser Gly Thr Ala Ile His Thr  
 135 140 145

gct cag ggc att gct gcg gca cgc aaa gaa gca ggc atg gac gca cag 595  
Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala Gly Met Asp Ala Gln  
150 155 160 165

cca gat gcg acc gag cag gca ctt gag ggt tcc cgt ggc gca agc gta 643  
Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser Arg Gly Ala Ser Val  
170 175 180

gat gga atc cgc gtt cat gca gtc cgc atg tcc ggc atg gtt gct cac 691  
Asp Gly Ile Pro Val His Ala Val Arg Met Ser Gly Met Val Ala His  
185 190 195

gag caa gtt atc ttt ggc acc cag ggt cag acc ttg acc atc aag cag 739  
Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr Leu Thr Ile Lys Gln  
200 205 210

gac tcc tat gat cgc aac tca ttt gca cca ggt gtc ttg gtg ggt gtg 787  
Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly Val Leu Val Gly Val  
215 220 225

cgc aac att gca cag cac cca ggc cta gtc gta gga ctt gag cat tac 835  
Arg Asn Ile Ala Gln His Pro Gly Leu Val Val Gly Leu Glu His Tyr  
230 235 240 245

cta ggc atg taaaggctca tttcagcagc ggg 867  
Leu Gly Leu

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<212> PRT  
<213> Corynebacterium glutamicum

<400> 34  
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Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala  
20 25 30

Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala  
35 40 45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu  
50 55 60

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly  
65 70 75 80

Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys  
85 90 95

Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val  
100 105 110

Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala  
115 120 125

Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly  
130 135 140

Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala  
145 150 155 160

Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser  
165 170 175

Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser



180	185	190
Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr		
195	200	205
Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly		
210	215	220
Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val		
225	230	235
240		
Gly Leu Glu His Tyr Leu Gly Leu		
245		

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 <211> 873  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(850)  
 <223> RXA00864

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 Val Ala Glu Gln Val 5  
 1  
 aaa ttg agc gtg gag ttg ata gcg tgc agt tct ttt act cca ccc gct 163  
 Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser Phe Thr Pro Pro Ala 20  
 10 15  
 gat gtt gag tgg tca act gat gtt gag ggc gcg gaa gca ctc gtc gag 211  
 Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala Glu Ala Leu Val Glu 35  
 25 30  
 ttt gcg ggt cgt gcc tgc tac gaa act ttt gat aag ccg aac cct cga 259  
 Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp Lys Pro Asn Pro Arg 50  
 40 45  
 act gct tcc aat gct gcg tat ctg cgc cac atc atg gaa gtg ggg cac 307  
 Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile Met Glu Val Gly His 65  
 55 60  
 act gct ttg ctt gag cat gcc aat gcc acg atg tat atc cga gcc att 355  
 Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met Tyr Ile Arg Gly Ile 85  
 70 75 80  
 tct cgg tcc gcg acc cat gaa ttg gtc cga cac cgc cat ttt tcc ttc 403  
 Ser Arg Ser Ala Thr His Glu Leu Val Arg His Arg His Phe Ser Phe 100  
 90 95  
 tct caa ctg tct cag cgt ttc gtg cac agc gga gaa tcg gaa gta gtg 451  
 Ser Gln L u Ser Gln Arg Phe Val His Ser Gly Glu Ser Glu Val Val 115  
 105 110  
 gtg ccc act ctc atc gat gaa gat ccg cag ttg cgt gaa ctt ttc atg 499

Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu Arg Glu Leu Phe Met  
 120 125 130

cac gcc atg gat gag tct cgg ttc gct ttc aat gag ctg ctt aat gcg 547  
 His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn Glu Leu Leu Asn Ala  
 135 140 145

ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca ctt tta agg aaa aag 595  
 Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala Leu Leu Arg Lys Lys  
 150 155 160 165

cag gct cgt caa gca gct cgc gct gtg ctg ccc aac gct aca gag tcc 643  
 Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro Asn Ala Thr Glu Ser  
 170 175 180

aga atc gtg gtg tct gga aac ttc cgc acc tgg agg cat ttc att ggc 691  
 Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp Arg His Phe Ile Gly  
 185 190 195

atg cga gcc agt gaa cat gca gac gtc gaa atc cgc gaa gta gcg gta 739  
 Met Arg Ala Ser Glu His Ala Asp Val Glu Ile Arg Glu Val Ala Val  
 200 205 210

gaa tgt tta aga aag ctg cag gta gca gcg cca act gtt ttc ggt gat 787  
 Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro Thr Val Phe Gly Asp  
 215 220 225

ttt gag att gaa act ttg gca gac gga tcg caa atg gca aca agc ccg 835  
 Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln Met Ala Thr Ser Pro  
 230 235 240 245

tat gtc atg gac ttt taacgcaaag ctcacaccca cga 873  
 Tyr Val Met Asp Phe  
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<210> 36  
 <211> 250  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 36  
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 20 25 30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp  
 35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile  
 50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met  
 65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His  
 85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly

100	105	110
Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu 115 120 125		
Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn 130 135 140		
Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala 145 150 155 160		
Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro 165 170 175		
Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp 180 185 190		
Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile 195 200 205		
Arg Glu Val Ala Val Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro 210 215 220		
Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln 225 230 235 240		
Met Ala Thr Ser Pro Tyr Val Met Asp Phe 245 250		

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 <211> 608  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA02843

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           Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser  
           1                  5                  10  
 acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158  
 Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp  
   15                  20                  25                  30  
 cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206  
 Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val  
                   35                  40                  45  
 acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc 254  
 Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr  
           50                  55                  60  
 gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt 302  
 Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val

65	70	75	
ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac			350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn			
80	85	90	
aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca			398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala			
95	100	105	110
ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc			446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser			
	115	120	125
gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg			494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val			
	130	135	140
cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat			542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp			
	145	150	155
ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg			590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr			
160	165	170	
ctc ggc gct tcc atg gtt			608
Leu Gly Ala Ser Met Val			
175	180		

&lt;210&gt; 38

&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 38

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Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser			
20	25	30	
Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg			
35	40	45	
Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr			
50	55	60	
Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg			
65	70	75	80
Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val			
85	90	95	
Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr			
100	105	110	
Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp			
115	120	125	

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile  
 130 135 140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr  
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Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly  
 165 170 175

Ala Ser Met Val  
 180

<210> 39  
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 <222> (101)..(1120)  
 <223> RXN00355

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ggtcctgatg aaagagatgt cccgaatca tcactaagt atg cat ctc ggt aag 115  
 Met His Leu Gly Lys  
 1 5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163  
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met  
 10 15 20

acc aac atc cgc gta gct atc gtg gcc tac gga aac ctg gga cgc agc 211  
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser  
 25 30 35

gtc gaa aag ctc att gcc aag cag ccc gac atg gac ctt gta gga atc 259  
 Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile  
 40 45 50

ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc 307  
 Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val  
 55 60 65

gcc gac gtg gac aag cag gcc gac gac gtg gac gtg ctg ttc ctg tgc 355  
 Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys  
 70 75 80 85

atg gcc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag 403  
 Met Gly Ser Ala Thr Asp Ile Prc Glu Gln Ala Pro Lys Phe Ala Gln  
 90 95 100

ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc 451  
 Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg  
 105 110 115

cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc gcc aac gtt gca 499  
 His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala  
 120 125 130

ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc 547  
 Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val  
 135 140 145

tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc 595  
 Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly  
 150 155 160 165

cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc 643  
 Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly  
 170 175 180

gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa 691  
 Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu  
 185 190 195

aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac 739  
 Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His  
 200 205 210

aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc 787  
 Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile  
 215 220 225

gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc 835  
 Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val  
 230 235 240 245

gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc 883  
 Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly  
 250 255 260

atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc 931  
 Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe  
 265 270 275

aac cac acc gtg gaa tac atc ctc aag ctg gac cga aac cca gat ttc 979  
 Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp Arg Asn Pro Asp Phe  
 280 285 290

acc gct tcc tca cag atc gct ttc ggt cgc gca gct cac cgc atg aag 1027  
 Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys  
 295 300 305

cag cag ggc caa agc gga gct ttc acc gtc ctc gaa gtt gct cca tac 1075  
 Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr  
 310 315 320 325

ctg ctc tcc cca gag aac ttg gac gat ctg atc gca cgc gac gtc 1120  
 Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile Ala Arg Asp Val  
 330 335 340

taatttagct cgaggggcaa gga 1143

&lt;210&gt; 40

&lt;211&gt; 340

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 40

Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu  
 1 5 10 15  
 Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly  
 20 25 30  
 Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met  
 35 40 45  
 Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr  
 50 55 60  
 Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp  
 65 70 75 80  
 Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala  
 85 90 95  
 Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His  
 100 105 110  
 Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala  
 115 120 125  
 Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe  
 130 135 140  
 Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln  
 145 150 155 160  
 His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu  
 165 170 175  
 Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser  
 180 185 190  
 Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr  
 195 200 205  
 Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala  
 210 215 220  
 Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe  
 225 230 235 240  
 Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp  
 245 250 255  
 Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly  
 260 265 270  
 Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp  
 275 280 285  
 Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala  
 290 295 300  
 Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu  
 305 310 315 320

Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile  
 325 330 335

Ala Arg Asp Val  
 340

<210> 41  
 <211> 958  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(958)  
 <223> FRXA00352

<400> 41  
 aatagatcag cgcacccgtg gtggaaccaa aaggctcaac aatacgaac gttagctttc 60  
 ggtagctgatg aaagagatgt cccatgaatca tcatctaagt atg cat ctc ggt aag 115  
 Met His Leu Gly Lys  
 1 5  
 ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163  
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met  
 10 15 20  
 acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211  
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser  
 25 30 35  
 gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259  
 Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile  
 40 45 50  
 ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc 307  
 Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val  
 55 60 65  
 gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc 355  
 Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys  
 70 75 80 85  
 atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag 403  
 Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln  
 90 95 100  
 ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc 451  
 Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg  
 105 110 115  
 cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca 499  
 His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala  
 120 125 130  
 ctg gtc tct acc gcc tgg gat cca gga atg ttc tcc atc aac cgc gtc 547  
 Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val  
 135 140 145  
 tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc 595



Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly  
 150 155 160 165  
 cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc 643  
 Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly  
 170 175 180  
 gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa 691  
 Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu  
 185 190 195  
 aag gcc cgc cgc ggc gaa gcc tgc gac ctt acc gga aag caa acc cac 739  
 Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His  
 200 205 210  
 aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc 787  
 Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile  
 215 220 225  
 gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc 835  
 Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val  
 230 235 240 245  
 gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc 883  
 Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly  
 250 255 260  
 atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc 931  
 Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe  
 265 270 275  
 aac cac acc qtg gaa tac atc ctc aag 958  
 Asn His Thr Val Glu Tyr Ile Leu Lys  
 280 285

&lt;210&gt; 42

&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 42

Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu  
 1 5 10 15  
 Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly  
 20 25 30  
 Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met  
 35 40 45  
 Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr  
 50 55 60  
 Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp  
 65 70 75 80  
 Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala  
 85 90 95  
 Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His

100	105	110
Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala 115 120 125		
Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe 130 135 140		
Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln 145 150 155 160		
His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu 165 170 175		
Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser 180 185 190		
Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr 195 200 205		
Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala 210 215 220		
Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe 225 230 235 240		
Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp 245 250 255		
Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly 260 265 270		
Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys 275 280 285		

<210> 43  
 <211> 1400  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1377)  
 <223> RXA00972

<400> 43	
cct gca cct ggt tgg cgt ttc cgc acc gga gaa gat gta aca atg gct Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala 1 5 10 15	48
aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca cgc aat Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn 20 25 30	96
gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg cct ctg Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu 35 40 45	144
cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc gac gag Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu	192

50	55	60	
gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc ggt gga Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly 65 70 75 80			240
cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag acc att Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile 85 90 95			288
gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca tcc atc Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile 100 105 110			336
aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc cgt atc Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile 115 120 125			384
acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg ttg gtt Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val 130 135 140			432
caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa cta gaa Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu 145 150 155 160			480
ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu 165 170 175			528
atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala 180 185 190			576
act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc ggt tcc Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser 195 200 205			624
gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg aac ctg Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu 210 215 220			672
gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc gaa ggc Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly 225 230 235 240			720
ttc aag ctg gca gca gaa cgc gtg ttg ggc ctg tac tca cag atc cac Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His 245 250 255			768
agc gaa ctg ggc gtt gcc ctt cct gaa ctg gat ctc ggt ggc gga tac Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr 260 265 270			816
ggc att gcc tat acc gca gct gaa gaa cca ctc aac gtc gca gaa gtt Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val 275 280 285			864
gcc tcc gac ctg ctc acc gca gtc gga aaa atg gca gcg gaa cta ggc Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly 290 295 300			912

atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc gca ggc 960  
 Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly  
 305 310 315 320  
 ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa gac gtc cac 1008  
 Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His  
 325 330 335  
 gta gac gac gac aaa acc cgc cgt tac atc gcc gtg gac gga ggc atg 1056  
 Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met  
 340 345 350  
 tcc gac aac atc cgc cca gca ctc tac ggg tcc gaa tac gac gcc cgc 1104  
 Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg  
 355 360 365  
 gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc atc gtg 1152  
 Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val  
 370 375 380  
 ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa atc tac 1200  
 Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr  
 385 390 395 400  
 cca tct cac atc acc agc ggc gac ttc ctt gca ctc gca gcc acc ggc 1248  
 Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly  
 405 410 415  
 gca tac tgc tac gcc alg agc tcc cgc tac aac gcc ttc aca cgg ccc 1296  
 Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro  
 420 425 430  
 gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg cgc cgc 1344  
 Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg  
 435 440 445  
 gaa acg ctc cac gac atc ctc tca cta gag gca taacgctttt cgacgcctga 1397  
 Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala  
 450 455  
 ccc 1400

<210> 44  
 <211> 459  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 44  
 Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala  
 1 5 10 15  
 Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn  
 20 25 30  
 Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu  
 35 40 45  
 Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu  
 50 55 60

Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly  
 65 70 75 80  
 Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile  
 85 90 95  
 Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile  
 100 105 110  
 Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile  
 115 120 125  
 Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val  
 130 135 140  
 Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu  
 145 150 155 160  
 Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu  
 165 170 175  
 Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala  
 180 185 190  
 Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser  
 195 200 205  
 Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu  
 210 215 220  
 Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly  
 225 230 235 240  
 Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His  
 245 250 255  
 Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr  
 260 265 270  
 Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val  
 275 280 285  
 Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly  
 290 295 300  
 Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly  
 305 310 315 320  
 Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His  
 325 330 335  
 Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met  
 340 345 350  
 Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg  
 355 360 365  
 Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val  
 370 375 380

Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr  
 385 390 395 400

Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly  
 405 410 415

Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro  
 420 425 430

Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg  
 435 440 445

Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala  
 450 455

<210> 45  
 <211> 2121  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2098)  
 <223> RXA02653

<400> 45  
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accggccgta ttcattccaa taaccgcgac agggaaacta atg ata ccg aag ccc 115  
 Met Ile Pro Lys Pro  
 1 5

gac gtg acc gac tta tat tta gag gac ctc tta aat gag ggt tgc gaa 163  
 Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu Asn Glu Gly Ser Glu  
 10 15 20

aag att cgg tcc gcc aag gat ctt tcc gaa ctt agg aca gtt cta aaa 211  
 Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu Arg Thr Val Leu Lys  
 25 30 35

gag gtt tcc tcc caa att cag gaa cga gct ggg aaa aaa gat gaa gaa 259  
 Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly Lys Lys Asp Glu Glu  
 40 45 50

tgg gga atg ggg gcc act tgg cgg gag ctg tac ccc agc atc gtg gaa 307  
 Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr Pro Ser Ile Val Glu  
 55 60 65

cgc gct tcc tac gaa ggg cgt gac agc cta atc gga ttt gat cac tta 355  
 Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile Gly Phe Asp His Leu  
 70 75 80 85

gcc cgg gaa atg gaa aga tta gcc ttc ggc cca cca tcc gaa agt ttt 403  
 Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro Pro Ser Glu Ser Phe  
 90 95 100

gaa tac ctc caa gaa ctc gta aaa tcc gga gtg gta gac atc act cac 451  
 Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val Val Asp Ile Thr His  
 105 110 115

ctg cat cgt ggc cgg gaa cca ctg aca gat tta gtt cgt gaa ctt gaa Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu Val Arg Glu Leu Glu 120 125 130	499
ata act gtg gtg ata gac gct gtt ctt ccc ccg ccg gga gta gtg cca Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro Gly Val Val Pro 135 140 145	547
ggc aca ttg gtg cac aat ttg gta aaa gag gga tat gcc aga atg cgt Gly Thr Leu Val His Asn Leu Val Lys Glu Gly Tyr Ala Arg Met Arg 150 155 160 165	595
cct ggg act cgg ggg tta gat gta gcg gct gac ggc acc gtt caa ggg Pro Gly Thr Arg Gly Leu Asp Val Ala Asp Gly Thr Val Gln Gly 170 175 180	643
caa cga cat ttg gct gca gtc gga cgg atg acg gaa gat gtg gtt ttg Gln Arg His Leu Ala Ala Val Gly Arg Met Thr Glu Asp Val Val Leu 185 190 195	691
ggt aat gac aca ttg tcg cga tca tta cat gac ata atc ccg aag tgg Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp Ile Ile Pro Lys Trp 200 205 210	739
gct cgt cga gtt atc cgc gac gcg agc acg tat ccc gat agg gta cat Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr Pro Asp Arg Val His 215 220 225	787
ggt act cca ccg ctt ccg gca cgg ttg gaa ccc tgg gcg gaa aag ctc Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro Trp Ala Glu Lys Leu 230 235 240 245	835
act tca gat ccg gcc aca tgc cgc cac ctg att gaa gaa ttc ggg agt Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile Glu Glu Phe Gly Ser 250 255 260	883
cct gtg aat gta ctc cat tca ggt tct atg cct cgt aat ata aat gag Pro Val Asn Val Leu His Ser Gly Ser Met Pro Arg Asn Ile Asn Glu 265 270 275	931
ttg gtt gac gcc ggc att cag atg ggg gtg gat act cga ata ttt ttt Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp Thr Arg Ile Phe Phe 280 285 290	979
gcc cgc aaa gcg aat aag ggt ctt acc ttc gtt gat gcc gtt aaa gac Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val Asp Ala Val Lys Asp 295 300 305	1027
acc ggt cat ggt gta gat gta gcc agt gaa cga gag tta tct cag gtg Thr Gly His Gly Val Asp Val Ala Ser Glu Arg Glu Leu Ser Gln Val 310 315 320 325	1075
ctt aat cgt gga gtc cca gga gag cgg atc att cta tcc gca gct atc Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile Leu Ser Ala Ala Ile 330 335 340	1123
aaa ccg gac aga cta ttg gca tta gcg atc gaa aat ggc gtg atc atc Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu Asn Gly Val Ile Ile 345 350 355	1171
tct gtg gat tcg cgt gat gaa tta gat cgc att tcg gct ttg gtt ggt	1219

Ser	Val	Asp	Ser	Arg	Asp	Glu	Leu	Asp	Arg	Ile	Ser	Ala	Leu	Val	Gly		
		360					365					370					
gac	cgc	gtt	gca	cga	gtt	gcg	cct	aga	gta	gct	cca	gat	cct	gca	gtc	1267	
Asp	Arg	Val	Ala	Arg	Val	Ala	Pro	Arg	Val	Ala	Pro	Asp	Pro	Ala	Val		
		375				380					385						
tta	cct	cca	act	aga	ttt	ggt	gag	cgt	gct	gca	gac	tgg	ggt	aat	cgg	1315	
Leu	Pro	Pro	Thr	Arg	Phe	Gly	Glu	Arg	Ala	Ala	Asp	Trp	Gly	Asn	Arg		
		390			395				400					405			
ctt	acc	gag	gtg	ata	ccc	ggc	gtg	gat	att	gtg	ggt	ctt	cac	gtt	cac	1363	
Leu	Thr	Glu	Val	Ile	Pro	Gly	Val	Asp	Ile	Val	Gly	Leu	His	Val	His		
				410				415						420			
ctc	cat	ggc	tat	gct	gca	aaa	gac	cgt	gct	ctg	gct	ctg	cag	gaa	tgt	1411	
Leu	His	Gly	Tyr	Ala	Ala	Lys	Asp	Arg	Ala	Leu	Ala	Leu	Gln	Glu	Cys		
			425				430						435				
tgc	caa	ctc	gtc	gat	tct	ctc	aga	gaa	tgc	ggg	cat	tcc	cca	cag	ttt	1459	
Cys	Gln	Leu	Val	Asp	Ser	Leu	Arg	Glu	Cys	Gly	His	Ser	Pro	Gln	Phe		
		440				445						450					
att	gac	ctt	gga	gga	ggg	gtg	cct	atg	agc	tac	att	gaa	tct	gag	gaa	1507	
Ile	Asp	Leu	Gly	Gly	Gly	Val	Pro	Met	Ser	Tyr	Ile	Glu	Ser	Glu	Glu		
	455				460						465						
gat	tgg	atc	cgt	tat	caa	tcc	gct	aaa	tct	gcg	act	tca	gcc	ggg	tat	1555	
Asp	Trp	Ile	Arg	Tyr	Gln	Ser	Ala	Lys	Ser	Ala	Thr	Ser	Ala	Gly	Tyr		
	470				475					480				485			
gcc	gaa	tcc	ttt	acg	tgg	aaa	gac	gat	cgc	tta	tct	aat	acg	tac	cgc	1603	
Ala	Glu	Ser	Phe	Thr	Trp	Lys	Asp	Asp	Pro	Leu	Ser	Asn	Thr	Tyr	Pro		
				490				495						500			
ttc	tat	cag	acc	cca	gtg	cgc	ggt	aat	tgg	ttg	aaa	gac	gtg	ctt	tct	1651	
Phe	Tyr	Gln	Thr	Pro	Val	Arg	Gly	Asn	Trp	Leu	Lys	Asp	Val	Leu	Ser		
			505				510						515				
aag	ggg	gta	gct	cag	atg	ctc	att	gac	cgc	gga	ttg	cgc	tta	cac	ata	1699	
Lys	Gly	Val	Ala	Gln	Met	Leu	Ile	Asp	Arg	Gly	Leu	Arg	Leu	His	Ile		
		520				525						530					
gag	cct	ggt	cga	agt	tta	cta	gat	ggg	tgt	ggc	gtc	act	ctt	gcc	gaa	1747	
Glu	Pro	Gly	Arg	Ser	Leu	Leu	Asp	Gly	Cys	Gly	Val	Thr	Leu	Ala	Glu		
	535				540					545							
gtt	gct	ttt	gtg	aaa	acc	cga	agt	gac	ggg	ttg	cct	cta	gtg	gga	ctg	1795	
Val	Ala	Phe	Val	Lys	Thr	Arg	Ser	Asp	Gly	Leu	Pro	Leu	Val	Gly	Leu		
	550				555				560					565			
gct	atg	aac	cga	acg	cag	tgc	cgc	act	aca	tcc	gat	gat	ttt	ctc	att	1843	
Ala	Met	Asn	Arg	Thr	Gln	Cys	Arg	Thr	Thr	Ser	Asp	Asp	Phe	Leu	Ile		
				570				575						580			
gat	ccc	ctg	cat	atc	act	gac	ggt	gat	gta	ggc	gag	gaa	atc	gaa	gca	1891	
Asp	Pro	Leu	His	Ile	Thr	Asp	Gly	Asp	Val	Gly	Glu	Glu	Ile	Glu	Ala		
			585				590						595				
tat	cta	gtg	ggt	gcc	tac	tgc	atc	gaa	gat	gag	ctg	att	tta	cgc	cgc	1939	
Tyr	Leu	Val	Gly	Ala	Tyr	Cys	Ile	Glu	Asp	Glu	Leu	Ile	Leu	Arg	Arg		



600	605	610	
cga atc cgc ttc ccg aga gga gtc aaa cca gga gat atc atc gga att			1987
Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly Asp Ile Ile Gly Il			
615	620	625	
cct aac acc gca gga tac ttc atg cat atc ttg gaa agt gca tcg cac			2035
Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu Glu Ser Ala Ser His			
630	635	640	645
caa atc ccg ttg gcg aaa aat gta gtg tgg ccg gag ggg cag tta gac			2083
Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro Glu Gly Gln Leu Asp			
650	655	660	
gat atc gat gcg gat taagacataa ccattcgcta atc			2121
Asp Ile Asp Ala Asp			
665			

<210> 46  
 <211> 666  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 46  
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 Asn Glu Gly Ser Glu Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu  
 20 25 30  
 Arg Thr Val Leu Lys Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly  
 35 40 45  
 Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr  
 50 55 60  
 Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile  
 65 70 75 80  
 Gly Phe Asp His Leu Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro  
 85 90 95  
 Pro Ser Glu Ser Phe Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val  
 100 105 110  
 Val Asp Ile Thr His Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu  
 115 120 125  
 Val Arg Glu Leu Glu Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro  
 130 135 140  
 Pro Gly Val Val Pro Gly Thr Leu Val His Asn Leu Val Lys Glu Gly  
 145 150 155 160  
 Tyr Ala Arg Met Arg Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp  
 165 170 175  
 Gly Thr Val Gln Gly Gln Arg His Leu Ala Ala Val Gly Arg Met Thr  
 180 185 190

Glu Asp Val Val Leu Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp  
 195 200 205  
 Ile Ile Pro Lys Trp Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr  
 210 215 220  
 Pro Asp Arg Val His Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro  
 225 230 235 240  
 Trp Ala Glu Lys Leu Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile  
 245 250 255  
 Glu Glu Phe Gly Ser Pro Val Asn Val Leu His Ser Gly Ser Met Pro  
 260 265 270  
 Arg Asn Ile Asn Glu Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp  
 275 280 285  
 Thr Arg Ile Phe Phe Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val  
 290 295 300  
 Asp Ala Val Lys Asp Thr Gly His Gly Val Asp Val Ala Ser Glu Arg  
 305 310 315 320  
 Glu Leu Ser Gln Val Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile  
 325 330 335  
 Leu Ser Ala Ala Ile Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu  
 340 345 350  
 Asn Gly Val Ile Ile Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile  
 355 360 365  
 Ser Ala Leu Val Gly Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala  
 370 375 380  
 Pro Asp Pro Ala Val Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala  
 385 390 395 400  
 Asp Trp Gly Asn Arg Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val  
 405 410 415  
 Gly Leu His Val His Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu  
 420 425 430  
 Ala Leu Gln Glu Cys Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly  
 435 440 445  
 His Ser Pro Gln Phe Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr  
 450 455 460  
 Ile Glu Ser Glu Glu Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala  
 465 470 475 480  
 Thr Ser Ala Gly Tyr Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu  
 485 490 495  
 Ser Asn Thr Tyr Pro Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu  
 500 505 510  
 Lys Asp Val Leu Ser Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly

515	520	525
Leu Arg Leu His Ile Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly		
530	535	540
Val Thr Leu Ala Glu Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu		
545	550	555
Pro Leu Val Gly Leu Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser		
565	570	575
Asp Asp Phe Leu Ile Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly		
580	585	590
Glu Glu Ile Glu Ala Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu		
595	600	605
Leu Ile Leu Arg Arg Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly		
610	615	620
Asp Ile Ile Gly Ile Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu		
625	630	635
Glu Ser Ala Ser His Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro		
645	650	655
Glu Gly Gln Leu Asp Asp Ile Asp Ala Asp		
660	665	

<210> 47  
 <211> 993  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(970)  
 <223> RXA01393

<400> 47  
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 agtaaaatga ttggttctta acatgggttta atatagcttc atg aac ccc att caa 115  
 Met Asn Pro Ile Gln  
 1 5  
 ctg gac act ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc 163  
 Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala  
 10 15 20  
 tcc tta gcc ctt tcc att tcc ccc tgc gcg gtg agt cag cgc gtt aaa 211  
 Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys  
 25 30 35  
 gct ctc gag cat cac gtg ggt cga gtg ttg gta tgc cgc acc caa ccg 259  
 Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro  
 40 45 50  
 gcc aaa gca acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa 307  
 Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys

55	60	65	
atg gtg ttg ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu 70 75 80 85			355
gct gaa atc ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr 90 95 100			403
tgg ttt cct ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr 105 110 115			451
ctc acg ctg cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg 120 125 130			499
cgt gga gat gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala 135 140 145			547
gga tgt gaa gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala 150 155 160 165			595
acc ccc tca ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp 170 175 180			643
gct gcg atg ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp 185 190 195			691
cgt gac ctg gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val 200 205 210			739
tcc att gtc ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly 215 220 225			787
ctt ggt tgg gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys 230 235 240 245			835
gca gga gaa gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met 250 255 260			883
tat tgg caa cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr 265 270 275			931
gac gcc gtc gtt gat gca gca atc gag gga ttg cgg cct tagttacttc Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu Arg Pro 280 285 290			980
tgaaaagggtt cag			993

<210> 48  
 <211> 290  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 48  
 Met Asn Pro Ile Gln Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly  
 1 5 10 15  
 Ser Phe Glu Gly Ala Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val  
 20 25 30  
 Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val  
 35 40 45  
 Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val  
 50 55 60  
 Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln  
 65 70 75 80  
 Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala  
 85 90 95  
 Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser  
 100 105 110  
 Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr  
 115 120 125  
 Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu  
 130 135 140  
 Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg  
 145 150 155 160  
 His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp  
 165 170 175  
 Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys  
 180 185 190  
 Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val  
 195 200 205  
 Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu  
 210 215 220  
 Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala  
 225 230 235 240  
 Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro  
 245 250 255  
 Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser  
 260 265 270  
 Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu  
 275 280 285  
 Arg Pro



Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro Leu Leu Cys Phe Ile	
170 175 180	
atc ctt gtt gca ttc ttg ggc ttt agc tgg gag aag ttc act gtt gat	691
Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp	
185 190 195	
tta tgg gcg cgt gat ggt ggc gtg ggc agc att ttt gat cag gtg cgc	739
Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile Phe Asp Gln Val Arg	
200 205 210	
ggc atc atg gtg tac acc gtg tgg gtg ttc atc ggt atc gaa ggt gca	787
Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile Glu Gly Ala	
215 220 225	
tcg gta tat tcc cgc cag gca cgc tca cgc agt gat gtc agc cga gct	835
Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser Asp Val Ser Arg Ala	
230 235 240 245	
acc gtg att ggt ttt gtg gct gtt ctc ctt ttg ctg gtg tcg att tct	883
Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu Leu Val Ser Ile Ser	
250 255 260	
tcg ctg agc ttc ggt gta ctg acc caa caa gag ctc gct gcg tta cca	931
Ser Leu Ser Phe Gly Val Leu Thr Gln Glu Leu Ala Ala Leu Pro	
265 270 275	
gat aat tcc atg gcg tcg gtg ctc gaa gct gtt gtt ggt cca tgg ggt	979
Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val Val Gly Pro Trp Gly	
280 285 290	
gcc gca ttg att tcg ttg ggt ctg tgt ctt tcg gtt ctt ggg gcc tat	1027
Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser Val Leu Gly Ala Tyr	
295 300 305	
gtg tcc tgg cag atg ctc tgc gca gaa cca ctg gcg ttg atg gca atg	1075
Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met	
310 315 320 325	
gat ggc ctc att cca agc aaa atc ggg gcc atc aac agc cgc ggt gct	1123
Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile Asn Ser Arg Gly Ala	
330 335 340	
gcc tgg atg gct cag ctg atc tcc acc atc gtg att cag att ttc atc	1171
Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val Ile Gln Ile Phe Ile	
345 350 355	
atc att ttc ttc ctc aac gag acc acc tac gtc tcc atg gtg caa ttg	1219
Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val Ser Met Val Gln Leu	
360 365 370	
gct acc aac cta tac ttg gtg cct tac ctg ttc tct gcc ttt tat ctg	1267
Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu	
375 380 385	
gtc atg ctg gca aca cgt gga aaa gga atc acc cac cca cat gcc ggc	1315
Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly	
390 395 400 405	
aca cgt ttt gat gat tcc ggt cca gag ata tcc cgc cga gaa aac cgc	1363
Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser Arg Arg Glu Asn Arg	

410	415	420	
aaa cac ctc atc gtc ggt tta gta gca acg gtg tat tca gtg tgg ctg			1411
Lys His Leu Ile Val Gly Leu Val Ala Thr Val Tyr Ser Val Trp Leu			
425	430	435	
ttt tac gct gca gaa ccg cag ttt gtc ctc ttc gga gcc atg gcg atg			1459
Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe Gly Ala Met Ala Met			
440	445	450	
ctt ccc ggc tta atc ccc tat gtg tgg aca agg att tat cgt ggc gaa			1507
Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg Ile Tyr Arg Gly Glu			
455	460	465	
cag gtg ttt aac cgc ttt gaa atc ggc gtg gtt gtt gtc ctg gtc gtt			1555
Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val Val Val Leu Val Val			
470	475	480	485
gct gcc agc gcg ggc gtt att ggt ttg gtc aac gga tca cta tcg ctt			1603
Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn Gly Ser Leu Ser Leu			
490	495	500	
taaacaccga aaccttcctg cta			1626

<210> 50  
 <211> 501  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 50  
 Val Asn Thr Gln Ser Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr  
 1 5 10 15  
 Ser Arg Thr Val Ser Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser  
 20 25 30  
 Thr Val Gly Ala Gly Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val  
 35 40 45  
 Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly  
 50 55 60  
 Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro  
 65 70 75 80  
 His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp  
 85 90 95  
 Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile  
 100 105 110  
 Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr  
 115 120 125  
 Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val  
 130 135 140  
 Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser  
 145 150 155 160



Gln Ala Ala Phe Leu Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro  
 165 170 175  
 Leu Leu Cys Phe Ile Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu  
 180 185 190  
 Lys Phe Thr Val Asp Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile  
 195 200 205  
 Phe Asp Gln Val Arg Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile  
 210 215 220  
 Gly Ile Glu Gly Ala Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser  
 225 230 235 240  
 Asp Val Ser Arg Ala Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu  
 245 250 255  
 Leu Val Ser Ile Ser Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu  
 260 265 270  
 Leu Ala Ala Leu Pro Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val  
 275 280 285  
 Val Gly Pro Trp Gly Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser  
 290 295 300  
 Val Leu Gly Ala Tyr Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu  
 305 310 315 320  
 Ala Leu Met Ala Met Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile  
 325 330 335  
 Asn Ser Arg Gly Ala Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val  
 340 345 350  
 Ile Gln Ile Phe Ile Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val  
 355 360 365  
 Ser Met Val Gln Leu Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe  
 370 375 380  
 Ser Ala Phe Tyr Leu Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr  
 385 390 395 400  
 His Pro His Ala Gly Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser  
 405 410 415  
 Arg Arg Glu Asn Arg Lys His Leu Ile Val Gly Leu Val Ala Thr Val  
 420 425 430  
 Tyr Ser Val Trp Leu Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe  
 435 440 445  
 Gly Ala Met Ala Met Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg  
 450 455 460  
 Ile Tyr Arg Gly Glu Gln Val Phe Asn Arg Phe Glu Il Gly Val Val  
 465 470 475 480  
 Val Val Leu Val Val Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn

485	490	495
Gly Ser Leu Ser Leu		
500		
<p>&lt;210&gt; 51          &lt;211&gt; 822          &lt;212&gt; DNA          &lt;213&gt; <i>Corynebacterium glutamicum</i></p> <p>&lt;220&gt;          &lt;221&gt; CDS          &lt;222&gt; (101)..(799)          &lt;223&gt; RXA01394</p> <p>&lt;400&gt; 51</p>		
<p>gagcaaagtg tccagttgaa tgggggttcat gaagctatat taaaccatgt taagaaccaa 60</p>		
tcattttact taagtacttc cataggtcac gatggatgatc	atg gaa atc ttc att	115
	Met Glu Ile Phe Ile	
	1 5	
aca ggt ctg ctt ttg ggg gcc agt ctt tta ctg tcc atc gga ccg cag		163
Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu Ser Ile Gly Pro Gln		
	10 15 20	
aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctc att gcg		211
Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala		
	25 30 35	
gtt ctt ctc gtg tgt tta att tct gac gtc ttt ttg ttc atc gcc ggc		259
Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly		
	40 45 50	
acc ttg ggc gtt gat ctt ttg tcc aat gcc gcg ccg atc gtg ctc gat		307
Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala Pro Ile Val Leu Asp		
	55 60 65	
att atg cgc tgg ggt ggc atc gct tac ctg tta tgg ttt gcc gtc atg		355
Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu Trp Phe Ala Val Met		
	70 75 80 85	
gca gcg aaa gac gcc atg aca aac aag gtg gaa gcg cca cag atc att		403
Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu Ala Pro Gln Ile Ile		
	90 95 100	
gaa gaa aca gaa cca acc gtg ccc gat gac acg cct ttg ggc ggt tcg		451
Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr Pro Leu Gly Gly Ser		
	105 110 115	
gcg gtg gcc act gac acg cgc aac cgg gtg cgg gtg gag gtg agc gtc		499
Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg Val Glu Val Ser Val		
	120 125 130	
gat aag cag cgg gtt tgg gta aag ccc atg ttg atg gca atc gtg ctg		547
Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu Met Ala Ile Val Leu		
	135 140 145	
acc tgg ttg aac ccg aat gcg tat ttg gac gcg ttt gtg ttt atc ggc		595
Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala Phe Val Phe Ile Gly		

150	155	160	165	
ggc gtc ggc gcg caa tac ggc gac acc gga cgg tgg att ttc gcc gct				643
Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg Trp Ile Phe Ala Ala				
170		175	180	
ggc gcg ttc gcg gca agc ctg atc tgg ttc ccg ctg gtg ggt ttc ggc				691
Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro Leu Val Gly Phe Gly				
185		190	195	
gca gca gca ttg tca cgc ccg ctg tcc agc ccc aag gtg tgg cgc tgg				739
Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro Lys Val Trp Arg Trp				
200		205	210	
atc aac gtc gtc gtg gca gtt gtg atg acc gca ttg gcc atc aaa ctg				787
Ile Asn Val Val Val Ala Val Val Met Thr Ala Leu Ala Ile Lys Leu				
215		220	225	
atg ttg atg ggt tagttttcgc gggttttgga atc				822
Met Leu Met Gly				
230				

&lt;210&gt; 52

&lt;211&gt; 233

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 52

Met	Glu	Ile	Phe	Ile	Thr	Gly	Leu	Leu	Leu	Gly	Ala	Ser	Leu	Leu	Leu
1				5					10					15	
Ser	Ile	Gly	Pro	Gln	Asn	Val	Leu	Val	Ile	Lys	Gln	Gly	Ile	Lys	Arg
			20					25					30		
Glu	Gly	Leu	Ile	Ala	Val	Leu	Leu	Val	Cys	Leu	Ile	Ser	Asp	Val	Phe
		35					40					45			
Leu	Phe	Ile	Ala	Gly	Thr	Leu	Gly	Val	Asp	Leu	Leu	Ser	Asn	Ala	Ala
	50					55				60					
Pro	Ile	Val	Leu	Asp	Ile	Met	Arg	Trp	Gly	Gly	Ile	Ala	Tyr	Leu	Leu
65				70					75					80	
Trp	Phe	Ala	Val	Met	Ala	Ala	Lys	Asp	Ala	Met	Thr	Asn	Lys	Val	Glu
			85					90						95	
Ala	Pro	Gln	Ile	Ile	Glu	Glu	Thr	Glu	Pro	Thr	Val	Pro	Asp	Asp	Thr
		100						105					110		
Pro	Leu	Gly	Gly	Ser	Ala	Val	Ala	Thr	Asp	Thr	Arg	Asn	Arg	Val	Arg
	115						120					125			
Val	Glu	Val	Ser	Val	Asp	Lys	Gln	Arg	Val	Trp	Val	Lys	Pro	Met	Leu
	130					135					140				
Met	Ala	Ile	Val	Leu	Thr	Trp	Leu	Asn	Pro	Asn	Ala	Tyr	Leu	Asp	Ala
145				150					155					160	
Phe	Val	Phe	Ile	Gly	Gly	Val	Gly	Ala	Gln	Tyr	Gly	Asp	Thr	Gly	Arg
				165					170					175	

Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro  
 180 185 190  
 Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro  
 195 200 205  
 Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met Thr Ala  
 210 215 220  
 Leu Ala Ile Lys Leu Met Leu Met Gly  
 225 230

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 <212> DNA  
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<220>  
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 <223> RXA00865

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 Met Ser Thr Gly Leu  
 1 5  
 aca gct aag acc gga gta gag cac ttc ggc acc gtt gga gta gca atg 163  
 Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr Val Gly Val Ala Met  
 10 15 20  
 gtt act cca ttc acg gaa tcc gga gac atc gat atc gct gct ggc cgc 211  
 Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp Ile Ala Ala Gly Arg  
 25 30 35  
 gaa gtc gcg gct tat ttg gtt gat aag ggc ttg gat tct ttg gtt ctc 259  
 Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu Asp Ser Leu Val Leu  
 40 45 50  
 gcg ggc acc act ggt gaa tcc cca acg aca acc gcc gct gaa aaa cta 307  
 Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr Ala Ala Glu Lys Leu  
 55 60 65  
 gaa ctg ctc aag gcc gtt cgt gag gaa gtt ggg gat cgg gcg aag ctc 355  
 Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly Asp Arg Ala Lys Leu  
 70 75 80 85  
 atc gcc ggt gtc gga acc aac aac acg cgg aca tct gtg gaa ctt gcg 403  
 Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr Ser Val Glu Leu Ala  
 90 95 100  
 gaa gct gct gct tct gct ggc gca gac ggc ctt tta gtt gta act cct 451  
 Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu Leu Val Val Thr Pro  
 105 110 115  
 tat tac tcc aag ccg agc caa gag gga ttg ctg gcg cac ttc ggt gca 499  
 Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu Ala His Phe Gly Ala

120	125	130	
att gct gca gca aca gag gtt cca att tgt ctc tat gac att cct ggt Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu Tyr Asp Ile Pro Gly 135 140 145			547
cgg tca ggt att cca att gag tct gat acc atg aga cgc ctg agt gaa Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu 150 155 160 165			595
tta cct acg att ttg gcg gtc aag gac gcc aag ggt gac ctc gtt gca Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala 170 175 180			643
gcc acg tca ttg atc aaa gaa acg gga ctt gcc tgg tat tca ggc gat Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp 185 190 195			691
gac cca cta aac ctt gtt tgg ctt gct ttg ggc gga tca ggt ttc att Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile 200 205 210			739
tcc gta att gga cat gca gcc ccc aca gca tta cgt gag ttg tac aca Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr 215 220 225			787
agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg gaa atc aac gcc aaa Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys 230 235 240 245			835
cta tca ccg ctg gta gct gcc caa ggt cgc ttg ggt gga gtc agc ttg Leu*Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu 250 255 260			883
gca aaa gct gct ctg cgt ctg cag ggc atc aac gta gga gat cct cga Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg 265 270 275			931
ctt cca att atg gct cca aat gag cag gaa ctt gag gct ctc cga gaa Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu Glu Ala Leu Arg Glu 280 285 290			979
gac atg aaa aaa gct gga gtt cta taaatatgaa tgattcccga aat Asp Met Lys Lys Ala Gly Val Leu 295 300			1026

&lt;210&gt; 54

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 54

Met	Ser	Thr	Gly	Leu	Thr	Ala	Lys	Thr	Gly	Val	Glu	His	Phe	Gly	Thr
1				5					10					15	

Val	Gly	Val	Ala	Met	Val	Thr	Pro	Phe	Thr	Glu	Ser	Gly	Asp	Ile	Asp
			20					25					30		

Ile	Ala	Ala	Gly	Arg	Glu	Val	Ala	Ala	Tyr	Leu	Val	Asp	Lys	Gly	Leu
	35						40					45			

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr  
 50 55 60  
 Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly  
 65 70 75 80  
 Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr  
 85 90 95  
 Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu  
 100 105 110  
 Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu  
 115 120 125  
 Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu  
 130 135 140  
 Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met  
 145 150 155 160  
 Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys  
 165 170 175  
 Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala  
 180 185 190  
 Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly  
 195 200 205  
 Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu  
 210 215 220  
 Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg  
 225 230 235 240  
 Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu  
 245 250 255  
 Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn  
 260 265 270  
 Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu  
 275 280 285  
 Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu  
 290 295 300

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXS02021

<400> 55

78

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 Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly  
 230 235 240 245  
 caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg 883  
 Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu  
 250 255 260  
 gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc 931  
 Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr  
 265 270 275  
 ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979  
 Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile  
 280 285 290  
 gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag 1027  
 Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu  
 295 300 305  
 cca gtt gcc cgc ctc aaa gct tgacccattt tcataaccag tgc 1071  
 Pro Val Ala Arg Leu Lys Ala  
 310 315

<210> 56  
 <211> 316  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 56  
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 Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile  
 20 25 30  
 Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr  
 35 40 45  
 Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val  
 50 55 60  
 Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val  
 65 70 75 80  
 Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu  
 85 90 95  
 Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His  
 100 105 110  
 Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys  
 115 120 125  
 Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg  
 130 135 140  
 Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met  
 145 150 155 160



Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg  
 165 170 175

Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu  
 180 185 190

Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu  
 195 200 205

Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly  
 210 215 220

Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu  
 225 230 235 240

Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile  
 245 250 255

Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val  
 260 265 270

Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg  
 275 280 285

Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu  
 290 295 300

Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala  
 305 310 315

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 <212> DNA  
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<220>  
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caccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115  
 Met Ser Thr Leu Glu  
 1 5

act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag 163  
 Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu  
 10 15 20

ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211  
 Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val  
 25 30 35

tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc 259  
 Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala  
 40 45 50

cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt	307
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly	
55 60 65	
cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag	355
His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu	
70 75 80 85	
gag ctc atc aag cgt ttt tcc gtc gtc ggc acc ctc gcc gcg caa	403
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln	
90 95 100	
acc cgg gtt ttc ttc tgc aac tcc ggc gcc gaa gca aac gag gct gct	451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala	
105 110 115	
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt	499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val	
120 125 130	
cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag	547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln	
135 140 145	
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc	595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe	
150 155 160 165	
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac	643
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn	
170 175 180	
cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg	691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr	
185 190 195	
ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg	739
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu	
200 205 210	
tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc	787
Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly	
215 220 225	
gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt	835
Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val	
230 235 240 245	
ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc	883
Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile	
250 255 260	
ggg gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc	931
Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly	
265 270 275	
aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc	979
Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala	
280 285 290	
aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc	1027

Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala  
 295 300 305  
 cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt 1075  
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val  
 310 315 320 325  
 gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc 1123  
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg  
 330 335 340  
 gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att 1171  
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile  
 345 350 355  
 ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg 1219  
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val  
 360 365 370  
 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca 1267  
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr  
 375 380 385  
 atc gca taaaggactc aaacttatga ctt 1296  
 Ile Ala  
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<210> 58  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 58  
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 Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp  
 20 25 30  
 Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn  
 35 40 45  
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln  
 50 55 60  
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val  
 65 70 75 80  
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala  
 85 90 95  
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu  
 100 105 110  
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg  
 115 120 125  
 Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu  
 130 135 140

Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro  
 145 150 155 160  
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys  
 165 170 175  
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro  
 180 185 190  
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys  
 195 200 205  
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp  
 210 215 220  
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln  
 225 230 235 240  
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly  
 245 250 255  
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu  
 260 265 270  
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val  
 275 280 285  
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe  
 290 295 300  
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala  
 305 310 315 320  
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly  
 325 330 335  
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe  
 340 345 350  
 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu  
 355 360 365  
 Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys  
 370 375 380  
 Ala Ile Ala Glu Thr Ile Ala  
 385 390

<210> 59  
 <211> 1908  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(985)  
 <223> RXC00733

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gtgaaattgt tgaatcccaa gagactgcgc aggcgcgaatc atg agt aat act gca	115
Met Ser Asn Thr Ala	
1 5	
ggc ccc cgc ggg cgt tcc cat cag gca gac gcc gcg ccg aat caa aag	163
Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala Pro Asn Gln Lys	
10 15 20	
gca cag aat ttc gga cca tct gcc aaa agg ctt ttc gga att cta ggc	211
Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu Phe Gly Ile Leu Gly	
25 30 35	
cat gac cgt aac acc tta att ttt gtt atc ttc cta gcc gtc ctg agc	259
His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe Leu Ala Val Leu Ser	
40 45 50	
gtt gga ctt acc gtc ttg ggc cca tgg ttg ctg ggt aaa gcc acc aac	307
Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu Gly Lys Ala Thr Asn	
55 60 65	
gtg gtg ttt gaa gga ttc cta tct aag cgc atg ccg gct ggt gcg tca	355
Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met Pro Ala Gly Ala Ser	
70 75 80 85	
aag gaa gat atc atc gcg cag ttg cag gct gca ggt aaa cat aat cag	403
Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala Gly Lys His Asn Gln	
90 95 100	
gct tcc atg atg gaa gac atg aac ctt gtt cca gcc tca gcc att gat	451
Ala Ser Met Met Glu Asp Met Asn Leu Val Pro Gly Ser Gly Ile Asp	
105 110 115	
ttt gaa aaa tta gcc atg atc ctc gga ctg gtg atc ggt gct tat ctc	499
Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu	
120 125 130	
atc ggt agc ctg ttg tgc ttg ttc cag gcg cgg atg ctc aac cgc atc	547
Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile	
135 140 145	
gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc	595
Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile	
150 155 160 165	
cac cgc cta ccg ctg agc tat ttc gat tcc atc aaa cgt ggt gat ctg	643
His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu	
170 175 180	
ctt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa	691
Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile Gly Gln Ser Leu Gln	
185 190 195	
caa acc ttg tca cag gcg atc act tcc cta ctg acc gtc atc ggt gtg	739
Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val	
200 205 210	
ttg gtg atg atg ttt atc atc tcc cca ctg ctc gca ctc gtg gcg ctg	787
Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu Ala Leu Val Ala Leu	
215 220 225	

gta tcc att ccg gtc acc atc gtg gtc act gtg gtg gtt gcg agc cgt 835  
 Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg  
 230 235 240 245

tcc cag aaa ctc ttt gcg gaa cag tgg aag cag acc ggt att ttg aat 883  
 Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln Thr Gly Ile Leu Asn  
 250 255 260

gcg cgc ctg gag gaa acc tac tct ggc cac gcc gtg gtt aag gtt ttc 931  
 Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala Val Val Lys Val Phe  
 265 270 275

gga cac caa aag gat gtt caa gaa gca ttc gag gaa gaa aat caa gct 979  
 Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu Glu Glu Asn Gln Ala  
 280 285 290

tgt gta taaggccagc tttggtgccc agt 1008  
 Cys Val  
 295

<210> 60  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 60  
 Met Ser Asn Thr Ala Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala  
 1 5 10 15

Ala Pro Asn Gln Lys Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu  
 20 25 30

Phe Gly Ile Leu Gly His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe  
 35 40 45

Leu Ala Val Leu Ser Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu  
 50 55 60

Gly Lys Ala Thr Asn Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met  
 65 70 75 80

Pro Ala Gly Ala Ser Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala  
 85 90 95

Gly Lys His Asn Gln Ala Ser Met Met Glu Asp Met Asn Leu Val Pro  
 100 105 110

Gly Ser Gly Ile Asp Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val  
 115 120 125

Ile Gly Ala Tyr Leu Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg  
 130 135 140

Met Leu Asn Arg Ile Val Gln Ser Ala Met His Arg Leu Arg Met Glu  
 145 150 155 160

Val Glu Glu Lys Ile His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile  
 165 170 175

Lys Arg Gly Asp Leu Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile

180	185	190
Gly Gln Ser Leu Gln Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu		
195	200	205
Thr Val Ile Gly Val Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu		
210	215	220
Ala Leu Val Ala Leu Val Ser Ile Pro Val Thr Ile Val Val Thr Val		
225	230	235
Val Val Ala Ser Arg Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln		
245	250	255
Thr Gly Ile Leu Asn Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala		
260	265	270
Val Val Lys Val Phe Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu		
275	280	285
Glu Glu Asn Gln Ala Cys Val		
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cct atg gct gcg ctg tct cgc atg gcg cgt cgt gag cac cga cag atc	96
Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile	
20 25 30	
act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca	144
Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro	
35 40 45	
ggg aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc	192
Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile	
50 55 60	
ggg gca act gtt gtt acc ggt cgc gac gcc aag gtg cac acc tcg ggc	240
Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly	
65 70 75 80	
cac ggc tac tcc gga gag ctg ttg ttc ttg tac aac gcc gct cgt ccg	288
His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro	
85 90 95	
aag aac gct atg cct gtc cac ggc gag tgg cgc cac ctg cgc gcc aac	336
Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn	

100 105 110  
 aag gaa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt 384  
 Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu  
 115 120 125  
 gca caa aac ggt gtt gtg gtt gat atg gtc aac ggt cgc gca 426  
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<210> 62  
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 <213> Corynebacterium glutamicum

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 35 40 45  
 Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile  
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 Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly  
 65 70 75 80  
 His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro  
 85 90 95  
 Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn  
 100 105 110  
 Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu  
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 ctctccgaga agacatgaaa aaagctggag ttctataaat atg aat gat tcc cga 115  
 Met Asn Asp Ser Arg  
 1 5



aat cgc ggc cgg aag gtt acc cgc aag gcg ggc cca cca gaa gct ggt	163
Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Glu Ala Gly	
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cag gaa aac cat ctg gat acc cct gtc ttt cag gca cca gat gct tcc	211
Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser	
25 30 35	
tct aac cag agc gct gta aaa gct gag acc gcc gga aac gac aat cgg	259
Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg	
40 45 50	
gat gct gcg caa ggt gct caa gga tcc caa gat tct cag ggt tcc cag	307
Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln	
55 60 65	
aac gct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac	355
Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn	
70 75 80 85	
cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga	403
Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly	
90 95 100	
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Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln	
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Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys	
120 125 130	
lcg atg cag ggt gcg gat ctg acc cag cgc ctg cca gag cca cca aag	547
Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys	
135 140 145	
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Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu	
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atc ggt cgc aac atg acc gtg ttt gag tac aac aac cgt ctg ctc atc	643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile	
170 175 180	
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Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp	
185 190 195	
ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc	739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val	
200 205 210	
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Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile	
215 220 225	
ccc tgg ctg ctg aag ctg cgc aac gat atc cca atc ttg gca tcc cgt	835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg	
230 235 240 245	

ttc acc ttg gct ctg att gca gct aag tgt aag gaa cac cgt cag cgt 883  
 Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg  
 250 255 260  
 ccg aag ctg atc gag gtc aac gag cag tcc aat gag gac cgc gga ccg 931  
 Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro  
 265 270 275  
 ttc aac att cgc ttc tgg gct gtt aac cac tcc atc cca gac tgc ctt 979  
 Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu  
 280 285 290  
 ggt ctt gct atc aag act cct gct ggt ttg gtc atc cac acc ggt gac 1027  
 Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp  
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 Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr  
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<210> 64  
 <211> 322  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 64

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 35 40 45  
 Gly Asn Asp Asn Arg Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp  
 50 55 60  
 Ser Gln Gly Ser Gln Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly  
 65 70 75 80  
 Asn Asn Asn Arg Asn Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly  
 85 90 95  
 Arg Arg Gly Ser Gly Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly  
 100 105 110  
 Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg  
 115 120 125  
 Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu  
 130 135 140  
 Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu  
 145 150 155 160  
 Gly Gly Ile Ser Glu Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn  
 165 170 175  
 Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser S r Gly

180							185					190				
Glu	Pro	Gly	Val	Asp	Leu	Ile	Leu	Pro	Asp	Phe	Gly	Pro	Ile	Glu	Asp	
		195					200				205					
His	Leu	His	Arg	Val	Asp	Ala	Leu	Val	Val	Thr	His	Gly	His	Glu	Asp	
		210			215						220					
His	Ile	Gly	Ala	Ile	Pro	Trp	Leu	Leu	Lys	Leu	Arg	Asn	Asp	Ile	Pro	
225				230						235				240		
Ile	Leu	Ala	Ser	Arg	Phe	Thr	Leu	Ala	Leu	Ile	Ala	Ala	Lys	Cys	Lys	
				245				250						255		
Glu	His	Arg	Gln	Arg	Pro	Lys	Leu	Ile	Glu	Val	Asn	Glu	Gln	Ser	Asn	
		260						265				270				
Glu	Asp	Arg	Gly	Pro	Phe	Asn	Ile	Arg	Phe	Trp	Ala	Val	Asn	His	Ser	
		275				280						285				
Ile	Pro	Asp	Cys	Leu	Gly	Leu	Ala	Ile	Lys	Thr	Pro	Ala	Gly	Leu	Val	
290						295				300						
Ile	His	Thr	Gly	Asp	Ile	Lys	Leu	Asp	Gln	Thr	Pro	Pro	Asp	Gly	Arg	
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Pro Thr																

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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1504)
<223> RXC02095
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Met Lys Thr Glu Gln
1 5

tcc caa aaa gca caa tta gcc cct aag aaa gca cct gaa aag cca caa 163
Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala Pro Glu Lys Pro Gln
10 15 20

cgc atc cgc caa ctt att tcc gtg gcg tgg cag cga cct tgg ctc acc 211
Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln Arg Pro Trp Leu Thr
25 30 35

tca ttc acc gta atc agc gct tta gct gca acg ttg ttt gaa ctt aca 259
Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr Leu Phe Glu Leu Thr
40 45 50

ctt cct ctt ttg acc ggt ggc gcc atc gat atc gcg ctc gga aat acc 307
Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile Ala Leu Gly Asn Thr

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tta agc gtg ttg acc agc gtc att gcc ctt atc gtg ctt ctc gcg ttg Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile Val Leu Leu Ala Leu 90 95 100			403
ctt cgc tat gcc agt caa ttt gga cgg cga tac acc gca ggc aag ctc Leu Arg Tyr Ala Ser Gln Phe Gly Arg Tyr Thr Ala Gly Lys Leu 105 110 115			451
agc atg ggg gta cag cat gat gtc cgg ctt aaa acg atg cgc tca ttg Ser Met Gly Val Gln His Asp Val Arg Leu Lys Thr Met Arg Ser Leu 120 125 130			499
cag aac ctc gat ggg cca ggt cag gac tct att cgc aca ggc caa gta Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile Arg Thr Gly Gln Val 135 140 145			547
gtc agt cgg tcc att tcg gat atc aac atg gtg caa agc ctt gtg gcg Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val Gln Ser Leu Val Ala 150 155 160 165			595
atg ttg ccg atg ttg atc gga aat gtg gtc aag ctt gtg ctc act ttg Met Leu Pro Met Leu Ile Gly Asn Val Val Lys Leu Val Leu Thr Leu 170 175 180			643
gtg atc atg ctg gct att tcc ccg ccg ctg acc atc atc gct gca gtg Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr Ile Ile Ala Ala Val 185 190 195			691
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atg gtt gag cag ctt ccg cag ctt gct ttg gtg gtc aac att gtt ggc Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val Val Asn Ile Val Gly 280 285 290			979
ggt ggc tat ttg gcc atg act ggt cac atc acg gtg ggc acg ttt gtg Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr Val Gly Thr Phe Val 295 300 305			1027

gcg ttt tct tcc tat ctc act agc ttg tgc gcg gtg gct agg tcc ctg 1075  
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 310 315 320 325

tgc ggc atg ctc atg cgc gtg cag ttg gcg ctg tct tct gtg gag cgc 1123  
 Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu Ser Ser Val Glu Arg  
 330 335 340

atc ttt gaa gtc att gat ctt cag cct gaa cgc acc gat cct gca cac 1171  
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 Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu Ser Phe Asn Asn Val  
 360 365 370

gat ttc cgt ggg att ctc aac ggt ttt gag ctg ggt gtt cag gcc ggt 1267  
 Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu Gly Val Gln Ala Gly  
 375 380 385

gaa acc gtt gtg ttg gtg ggc cct cca ggt tca ggc aag acc atg gct 1315  
 Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser Gly Lys Thr Met Ala  
 390 395 400 405

gtg cag ctt gct gga aac ttt tat caa cca gac agc ggc cac atc gcc 1363  
 Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp Ser Gly His Ile Ala  
 410 415 420

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 Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp Asp Leu Thr His Ser  
 425 430 435

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 Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp Glu Pro Phe Leu Tyr  
 440 445 450

tcc tcc tcc ata ccg cga gaa cat ctc gat ggg ttt gga tgt cag 1504  
 Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly Phe Gly Cys Gln  
 455 460 465

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&lt;210&gt; 66

&lt;211&gt; 468

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 66

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Pro Glu Lys Pro Gln Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln  
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Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr  
 35 40 45

L u Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile  
 50 55 60

Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg  
 65 70 75 80  
 Phe Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile  
 85 90 95  
 Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr  
 100 105 110  
 Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys  
 115 120 125  
 Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile  
 130 135 140  
 Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val  
 145 150 155 160  
 Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys  
 165 170 175  
 Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr  
 180 185 190  
 Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr  
 195 200 205  
 Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala  
 210 215 220  
 Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val  
 225 230 235 240  
 Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu  
 245 250 255  
 Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr  
 260 265 270  
 Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val  
 275 280 285  
 Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr  
 290 295 300  
 Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala  
 305 310 315 320  
 Val Ala Arg Ser Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu  
 325 330 335  
 Ser Ser Val Glu Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg  
 340 345 350  
 Thr Asp Pro Ala His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu  
 355 360 365  
 Ser Phe Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu  
 370 375 380

Gly Val Gln Ala Gly Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser  
 385 390 395 400

Gly Lys Thr Met Ala Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp  
 405 410 415

Ser Gly His Ile Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp  
 420 425 430

Asp Leu Thr His Ser Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp  
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Glu Pro Phe Leu Tyr Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly  
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Phe Gly Cys Gln  
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 <222> (34)..(272)  
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 Met Asn Asp Leu Ala Ala Glu Gly Glu Asn  
 1 5 10

gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc 161  
 Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe  
 15 20 25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209  
 Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile  
 30 35 40

ccg atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct 257  
 Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala  
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tca cgc gag tcc ctg taaaagcatt tcgcttttcg acg 295  
 Ser Arg Glu Ser Leu  
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<210> 63  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys  
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35 40 45

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<212> DNA  
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Met Leu Asp Asn Ser  
1 5  
ttt tac acc gca gag gtt cag ggc cca tac gaa acc gct tcc att ggc 163  
Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu Thr Ala Ser Ile Gly  
10 15 20  
cgg ctc gaa ctc gaa gaa ggg ggt gtg att gag gat tgc tgg ttg gct 211  
Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu Asp Cys Trp Leu Ala  
25 30 35  
tac gct aca gct gga acg ctc aac gag gac aag tcc aac gcc atc ctc 259  
Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys Ser Asn Ala Ile Leu  
40 45 50  
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Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr Trp Phe Gln Gln Tyr  
55 60 65  
atc ggc act gat cat gcg ctg gat cca tca aag tat ttc atc atc tcc 355  
Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys Tyr Phe Ile Ile Ser  
70 75 80 85  
atc aac caa atc ggt aat ggt ttg tcg gtc tcc cct gcc aac acg gct 403  
Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser Pro Ala Asn Thr Ala  
90 95 100  
gat gac agc atc tcg atg tcc aag ttc ccg aat gtt cgc att ggt gat 451  
Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn Val Arg Ile Gly Asp  
105 110 115  
gat gtc gtt gcc cag gac cgg ctc ttg cgc caa gag ttt ggt att acc 499  
Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln Glu Phe Gly Ile Thr  
120 125 130  
gag ctc ttt gcc gtc gtt ggt ggt tcg atg ggt gcg cag caa acc tat 547



Glu	Leu	Phe	Ala	Val	Val	Gly	Gly	Ser	Met	Gly	Ala	Gln	Gln	Thr	Tyr		
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Glu	Trp	Ile	Val	Arg	Phe	Pro	Asp	Gln	Val	His	Arg	Ala	Ala	Pro	Ile	165	
150					155					160							
gcg	ggc	act	gcg	aag	aac	act	cct	cat	gat	ttc	atc	ttc	acc	cag	act	643	
Ala	Gly	Thr	Ala	Lys	Asn	Thr	Pro	His	Asp	Phe	Ile	Phe	Thr	Gln	Thr	180	
				170					175								
ctt	aat	gag	acc	gtt	gag	gcc	gat	cca	ggg	ttc	aat	ggc	ggc	gaa	tac	691	
Leu	Asn	Glu	Thr	Val	Glu	Ala	Asp	Pro	Gly	Phe	Asn	Gly	Gly	Glu	Tyr	195	
			185					190					195				
tcc	tcc	cat	gaa	gag	gta	gct	gat	gga	ctt	cgc	cgt	caa	tcg	cat	ctt	739	
Ser	Ser	His	Glu	Glu	Val	Ala	Asp	Gly	Leu	Arg	Arg	Gln	Ser	His	Leu	210	
		200					205					210					
tgg	gct	gcc	atg	gga	ttt	tcc	aca	gag	ttc	tgg	aag	cag	gag	gca	tgg	787	
Trp	Ala	Ala	Met	Gly	Phe	Ser	Thr	Glu	Phe	Trp	Lys	Gln	Glu	Ala	Trp	225	
	215					220					225						
cgt	cgc	ctg	gga	ctt	gaa	agt	aag	gag	tca	gtg	ctc	gcg	gac	ttc	ctg	835	
Arg	Arg	Leu	Gly	Leu	Glu	Ser	Lys	Glu	Ser	Val	Leu	Ala	Asp	Phe	Leu	245	
230					235					240							
gat	ccg	ctg	ttc	atg	tcc	atg	gat	cct	aat	acc	ttg	ctc	aac	aac	gct	883	
Asp	Pro	Leu	Phe	Met	Ser	Met	Asp	Pro	Asn	Thr	Leu	Leu	Asn	Asn	Ala	260	
				250					255								
tgg	aag	tgg	cag	cat	ggc	gat	gtc	tct	cgc	cac	acc	ggc	ggc	gac	ttg	931	
Trp	Lys	Trp	Gln	His	Gly	Asp	Val	Ser	Arg	His	Thr	Gly	Gly	Asp	Leu	275	
			265					270					275				
gca	gcg	gct	ctt	ggc	cga	gtg	aag	gct	aag	acc	ttc	gtt	atg	ccc	atc	979	
Ala	Ala	Ala	Leu	Gly	Arg	Val	Lys	Ala	Lys	Thr	Phe	Val	Met	Pro	Ile	290	
		280					285					290					
agc	gag	gac	atg	ttc	ttt	cct	gtt	cgt	gac	tgt	gcc	gca	gaa	caa	gca	1027	
Ser	Glu	Asp	Met	Phe	Phe	Pro	Val	Arg	Asp	Cys	Ala	Ala	Glu	Gln	Ala	305	
	295					300					305						
ctc	atc	cca	ggc	agc	gag	ctt	cga	gtg	atc	gaa	gac	atc	gcc	ggc	cac	1075	
Leu	Ile	Pro	Gly	Ser	Glu	Leu	Arg	Val	Ile	Glu	Asp	Ile	Ala	Gly	His	325	
310					315					320							
ctt	ggg	ctt	ttt	aac	gtc	tct	gag	aat	tac	atc	cca	cag	atc	gac	aaa	1123	
Leu	Gly	Leu	Phe	Asn	Val	Ser	Glu	Asn	Tyr	Ile	Pro	Gln	Ile	Asp	Lys	340	
				330					335								
aat	ctg	aaa	gag	ctg	ttc	gag	agc	taa	ac	act	ga	tgt	caa	ag	gag	cct	1170
Asn	Leu	Lys		Leu	Phe	Glu	Ser										
			345														

&lt;210&gt; 70

&lt;211&gt; 349

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 70

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 1 5 10 15  
 Thr Ala Ser Ile Gly Arg Leu Glu Leu Glu Gly Gly Val Ile Glu  
 20 25 30  
 Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys  
 35 40 45  
 Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr  
 50 55 60  
 Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys  
 65 70 75 80  
 Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser  
 85 90 95  
 Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn  
 100 105 110  
 Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln  
 115 120 125  
 Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly  
 130 135 140  
 Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His  
 145 150 155 160  
 Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe  
 165 170 175  
 Ile Phe Thr Cln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe  
 180 185 190  
 Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg  
 195 200 205  
 Arg Gln Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp  
 210 215 220  
 Lys Gln Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val  
 225 230 235 240  
 Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr  
 245 250 255  
 Leu Leu Asn Asn Ala Trp Lys Trp Gln His Gly Asp Val Ser Arg His  
 260 265 270  
 Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr  
 275 280 285  
 Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys  
 290 295 300  
 Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu  
 305 310 315 320

Asp Ile Ala Gly His Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile  
 325 330 335

Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser  
 340 345

<210> 71

<211> 1254

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1231)

<223> RXN00403

<400> 71

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 Met Pro Thr Leu Ala  
 1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163  
 Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu  
 10 15 20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211  
 Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly  
 25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259  
 Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu  
 40 45 50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307  
 His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu  
 55 60 65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355  
 Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys  
 70 75 80 85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403  
 Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met  
 90 95 100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451  
 His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile  
 105 110 115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499  
 Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile  
 120 125 130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547  
 Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr  
 135 140 145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595

Leu	Glu	Trp	Ala	Ala	Met	Tyr	Pro	Glu	Thr	Val	Gly	Ala	Ala	Ala	Val	
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ctt	gca	gtt	tct	gca	cgc	gcc	agc	gcc	tgg	caa	atc	ggc	att	caa	tcc	643
Leu	Ala	Val	Ser	Ala	Arg	Ala	Ser	Ala	Trp	Gln	Ile	Gly	Ile	Gln	Ser	
				170					175					180		
gcc	caa	att	aag	gcg	att	gaa	aac	gac	cac	cac	tgg	cac	gaa	ggc	aac	691
Ala	Gln	Ile	Lys	Ala	Ile	Glu	Asn	Asp	His	His	Trp	His	Glu	Gly	Asn	
			185					190					195			
tac	tac	gaa	tcc	ggc	tgc	aac	cca	gcc	acc	gga	ctc	ggc	gcc	gcc	cga	739
Tyr	Tyr	Glu	Ser	Gly	Cys	Asn	Pro	Ala	Thr	Gly	Leu	Gly	Ala	Ala	Arg	
		200					205					210				
cgc	atc	gcc	cac	ctc	acc	tac	cgt	ggc	gaa	cta	gaa	atc	gac	gaa	cgc	787
Arg	Ile	Ala	His	Leu	Thr	Tyr	Arg	Gly	Glu	Leu	Glu	Ile	Asp	Glu	Arg	
	215					220					225					
ttc	ggc	acc	aaa	gcc	caa	aag	aac	gaa	aac	cca	ctc	ggt	ccc	tac	cgc	835
Phe	Gly	Thr	Lys	Ala	Gln	Lys	Asn	Glu	Asn	Pro	Leu	Gly	Pro	Tyr	Arg	
	230				235					240					245	
aag	ccc	gac	cag	cgc	ttc	gcc	gtg	gaa	tcc	tac	ttg	gac	tac	caa	gca	883
Lys	Pro	Asp	Gln	Arg	Phe	Ala	Val	Glu	Ser	Tyr	Leu	Asp	Tyr	Gln	Ala	
				250					255					260		
gac	aag	cta	gta	cag	cgt	ttc	gac	gcc	ggc	tcc	tac	gtc	ttg	ctc	acc	931
Asp	Lys	Leu	Val	Gln	Arg	Phe	Asp	Ala	Gly	Ser	Tyr	Val	Leu	Leu	Thr	
			265					270					275			
gac	gcc	ctc	aac	cgc	cac	gac	att	ggt	cgc	gac	cgc	gga	ggc	ctc	aac	979
Asp	Ala	Leu	Asn	Arg	His	Asp	Ile	Gly	Arg	Asp	Arg	Gly	Gly	Leu	Asn	
		280					285					290				
aag	gca	ctc	gaa	tcc	atc	aaa	gtt	cca	gtc	ctt	gtc	gca	ggc	gta	gat	1027
Lys	Ala	Leu	Glu	Ser	Ile	Lys	Val	Pro	Val	Leu	Val	Ala	Gly	Val	Asp	
	295					300					305					
acc	gat	att	ttg	tac	ccc	tac	cac	cag	caa	gaa	cac	ctc	tcc	aga	aac	1075
Thr	Asp	Ile	Leu	Tyr	Pro	Tyr	His	Gln	Gln	Glu	His	Leu	Ser	Arg	Asn	
	310				315					320					325	
ctg	gga	aat	cta	ctg	gca	atg	gca	aaa	atc	gta	tcc	cct	gtc	ggc	cac	1123
Leu	Gly	Asn	Leu	Leu	Ala	Met	Ala	Lys	Ile	Val	Ser	Pro	Val	Gly	His	
				330					335					340		
gat	gct	ttc	ctc	acc	gaa	agc	cgc	caa	atg	gat	cgc	atc	gtg	agg	aac	1171
Asp	Ala	Phe	Leu	Thr	Glu	Ser	Arg	Gln	Met	Asp	Arg	Ile	Val	Arg	Asn	
			345					350					355			
ttc	ttc	agc	ctc	atc	tcc	cca	gac	gaa	gac	aac	cct	tgc	acc	tac	atc	1219
Phe	Phe	Ser	Leu	Ile	Ser	Pro	Asp	Glu	Asp	Asn	Pro	Ser	Thr	Tyr	Ile	
		360					365					370				
gag	ttc	tac	atc	taataggtat	ttacgacaaa	tag										1254
Glu	Phe	Tyr	Ile													
			375													

&lt;210&gt; 72

&lt;211&gt; 377

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 72

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Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
 1           5           10           15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
          20           25           30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
          35           40           45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
          50           55           60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65           70           75           80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
          85           90           95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
          100           105           110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
          115           120           125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
          130           135           140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
          145           150           155           160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
          165           170           175

Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
          180           185           190

Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
          195           200           205

Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
          210           215           220

Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
          225           230           235           240

Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
          245           250           255

Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
          260           265           270

Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
          275           280           285

Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
          290           295           300

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Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
305 310 315 320

His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
325 330 335

Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
340 345 350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn  
355 360 365

Pro Ser Thr Tyr Ile Glu Phe Tyr Ile  
370 375

<210> 73

<211> 1210

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1210)

<223> FRXA00403

<400> 73

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aagtttttagt cttgtccacc cagaacaggc gggtatttttc atg ccc acc ctc gcg 115  
Met Pro Thr Leu Ala  
1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163  
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu  
10 15 20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211  
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly  
25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259  
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu  
40 45 50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307  
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu  
55 60 65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355  
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys  
70 75 80 85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403  
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met  
90 95 100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451  
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile  
105 110 115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile 120 125 130	499
acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr 135 140 145	547
cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Val 150 155 160 165	595
ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser 170 175 180	643
gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn 185 190 195	691
tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg 200 205 210	739
cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg 215 220 225	787
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg 230 235 240 245	835
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala 250 255 260	883
gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr 265 270 275	931
gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn 280 285 290	979
aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp 295 300 305	1027
acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn 310 315 320 325	1075
ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His 330 335 340	1123
gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn 345 350 355	1171

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 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser  
 360 365 370

1210

<210> 74  
 <211> 370  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 74  
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 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
 35 40 45  
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
 50 55 60  
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
 65 70 75 80  
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr  
 85 90 95  
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe  
 100 105 110  
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu  
 115 120 125  
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met  
 130 135 140  
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val  
 145 150 155 160  
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln  
 165 170 175  
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His  
 180 185 190  
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly  
 195 200 205  
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu  
 210 215 220  
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro  
 225 230 235 240  
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr  
 245 250 255  
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser  
 260 265 270



Tyr Val Leu L u Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp  
 275 280 285  
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu  
 290 295 300  
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
 305 310 315 320  
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
 325 330 335  
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
 340 345 350  
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn  
 355 360 365  
 Pro Ser  
 370

<210> 75  
 <211> 687  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(664)  
 <223> RXS03158

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 Leu His Ser Thr Thr  
 1 5  
 aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163  
 Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr  
 10 15 20  
 aac gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc 211  
 Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile  
 25 30 35  
 gga ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc 259  
 Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu  
 40 45 50  
 aag acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307  
 Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys  
 55 60 65  
 atc gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac 355  
 Ile Ala Glu Phe Leu Asp S r Arg Pro Glu Val Ser Thr Val Leu Tyr  
 70 75 80 85  
 cca ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg 403

Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met  
                             90                            95                            100

aag cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451  
 Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu  
                             105                            110                            115

gca gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag 499  
 Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu  
                             120                            125                            130

tcc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547  
 Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr  
                             135                            140                            145

cac cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595  
 His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val  
                             150                            155                            160                            165

cgc atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643  
 Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val  
                             170                            175                            180

gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687  
 Glu Gln Ala Leu Asn Asn Leu  
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 <211> 188  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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                             20                            25                            30

Met Gln Gly Gly Ile Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu  
                             35                            40                            45

Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys  
                             50                            55                            60

Asp Asn Ala Glu Lys Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val  
                             65                            70                            75                            80

Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val  
                             85                            90                            95

Ala Ala Lys Gln Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe  
                             100                            105                            110

Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu  
                             115                            120                            125

Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His  
                             130                            135                            140

Pro Ala Thr Met Thr His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val  
145 150 155 160

Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp  
165 170 175

Leu Leu Ala Asp Val Glu Gln Ala Leu Asn Asn Leu  
180 185

<210> 77

<211> 617

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(594)

<223> FRXA00254

<400> 77

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Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys  
1 5 10 15

tac atc gga gga cac tcc gac gtt gtt ggc ggc ctt gtg gtt acc aac 96  
Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn  
20 25 30

qac caq qaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc gga 144  
Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly  
35 40 45

ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc aag 192  
Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys  
50 55 60

acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag atc 240  
Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile  
65 70 75 80

gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac cca 288  
Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro  
85 90 95

ggc ctg aag cac cac cca ggc cac gaa gtc gca gcg aag cag atg aag 336  
Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys  
100 105 110

cgc ttc ggc cgc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa gca 384  
Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala  
115 120 125

gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag tcc 432  
Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser  
130 135 140

ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc cac 480  
Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His  
145 150 155 160

cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg cgc 528  
 Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg  
                   165                  170                  175

atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc gag 576  
 Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu  
                   180                  185                  190

cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 617  
 Gln Ala Leu Asn Asn Leu  
                   195

<210> 78  
 <211> 198  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 78  
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Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn  
                   20                  25                  30

Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly  
                   35                  40                  45

Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys  
   50                  55                  60

Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile  
   65                  70                  75                  80

Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro  
                   85                  90                  95

Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys  
                   100                  105                  110

Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala  
                   115                  120                  125

Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser  
   130                  135                  140

Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His  
   145                  150                  155                  160

Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg  
                   165                  170                  175

Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu  
                   180                  185                  190

Gln Ala Leu Asn Asn Leu  
                   195

<210> 79  
 <211> 1170

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1147)

&lt;223&gt; RXA02532

&lt;400&gt; 79

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tgtgcaagcg ggacggccag ccagaactcc tgggtgcgccg atg aac cca cct atc 115
                                         Met Asn Pro Pro Ile
                                         1           5

acg ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg cgc 163
Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu Lys Ala Tyr Gly Arg
                        10                        15                        20

gat ggc aat gat gga tgg ggt gca ttt gag gct gcc atg gga act cta 211
Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala Ala Met Gly Thr Leu
                        25                        30                        35

gat ggt ggg ttc gcg gta tct tat tct tca ggt ttg gca gcg gca acg 259
Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly Leu Ala Ala Ala Thr
                        40                        45                        50

tcg att gct gat ttg gtt cct act ggt ggc aca gtt gtt tta cct aaa 307
Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr Val Val Leu Pro Lys
                        55                        60                        65

gct gcc tat tat ggc gtg acc aat att ttc gcc agg atg gaa gcc cgc 355
Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala Arg Met Glu Ala Arg
                        70                        75                        80                        85

gga agg ctg aag gtt cga act gtt gat gca gac aat acc gaa gaa gtg 403
Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp Asn Thr Glu Glu Val
                        90                        95                        100

att gct gct gct caa ggt gca gat gtg gtg tgg gtg gaa tcg atc gct 451
Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp Val Glu Ser Ile Ala
                        105                        110                        115

aat ccg acg atg gtg gta gct gat atc cct gca ata gtc gac ggt gtg 499
Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala Ile Val Asp Gly Val
                        120                        125                        130

cgt ggg ctt gga gtt ttg act gtc gtt gac gcg act ttc gca acg cca 547
Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala Thr Phe Ala Thr Pro
                        135                        140                        145

ctt cgt caa cgt cca ttg gaa ctt ggt gct gat att gtg ctt tac tcg 595
Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp Ile Val Leu Tyr Ser
                        150                        155                        160                        165

gca acc aaa ctt atc ggt gga cac tct gat ctt ctt ctt gga gtc gca 643
Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu Leu Leu Gly Val Ala
                        170                        175                        180

gtg tgc aag tct gag cac cat gcg cag ttt ctt gcc act cac cgt cat 691
Val Cys Lys Ser Glu His His Ala Gln Phe Leu Ala Thr His Arg His

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185					190					195						
gat	cat	ggt	tca	gtg	ccg	gga	ggt	ctt	gaa	gcg	ttt	ctt	gct	ctc	cgt	739
Asp	His	Gly	Ser	Val	Pro	Gly	Gly	Leu	Glu	Ala	Phe	Leu	Ala	Leu	Arg	
		200					205					210				
gga	ttg	tat	tcc	ttg	gcg	gtg	cgt	ctt	gat	cga	gca	gaa	tcc	aac	gca	787
Gly	Leu	Tyr	Ser	Leu	Ala	Val	Arg	Leu	Asp	Arg	Ala	Glu	Ser	Asn	Ala	
	215					220					225					
gca	gaa	ctc	tcg	cgg	cga	ctt	aac	gcg	cat	cct	tcg	gtt	acc	cgc	gtc	835
Ala	Glu	Leu	Ser	Arg	Arg	Leu	Asn	Ala	His	Pro	Ser	Val	Thr	Arg	Val	
230				235				240						245		
aat	tat	cca	gga	ctt	cct	gat	gat	ccc	caa	cat	gaa	aaa	gcc	gtg	cga	883
Asn	Tyr	Pro	Gly	Leu	Pro	Asp	Asp	Pro	Gln	His	Glu	Lys	Ala	Val	Arg	
			250					255						260		
gtc	cta	ccc	tct	gga	tgt	gga	aac	atg	ttg	tca	ttt	gag	ctt	gat	gca	931
Val	Leu	Pro	Ser	Gly	Cys	Gly	Asn	Met	Leu	Ser	Phe	Glu	Leu	Asp	Ala	
		265					270					275				
aca	cct	gaa	cga	act	gat	gag	att	ctc	gaa	agc	ctg	tca	ctt	tta	acc	979
Thr	Pro	Glu	Arg	Thr	Asp	Glu	Ile	Leu	Glu	Ser	Leu	Ser	Leu	Leu	Thr	
		280				285					290					
cac	gcg	acc	agt	tgg	gga	ggt	gtg	gaa	aca	gcc	att	gaa	cgt	cgc	acc	1027
His	Ala	Thr	Ser	Trp	Gly	Gly	Val	Glu	Thr	Ala	Ile	Glu	Arg	Arg	Thr	
	295				300						305					
agg	cgg	gat	gcc	gaa	gtg	gtg	gca	gaa	gta	ccg	atg	act	ctt	tgc	cgc	1075
Arg	Arg	Asp	Ala	Glu	Val	Val	Ala	Glu	Val	Pro	Met	Thr	Leu	Cys	Arg	
310				315				320						325		
gtt	tcc	gta	cga	att	gaa	gac	gtt	gaa	gat	cta	tgg	gaa	gac	ctc	aac	1123
Val	Ser	Val	Gly	Ile	Glu	Asp	Val	Glu	Asp	Leu	Trp	Glu	Asp	Leu	Asn	
			330					335						340		
gcc	tca	atc	gac	aaa	gtt	ctg	ggt	tagaactcgt	agccagtaac	cag						1170
Ala	Ser	Ile	Asp	Lys	Val	Leu	Gly									
			345													

&lt;210&gt; 80

&lt;211&gt; 349

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 80

Met	Asn	Pro	Pro	Ile	Thr	Leu	Ser	Ser	Thr	Tyr	Val	His	Asp	Ser	Glu
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Lys	Ala	Tyr	Gly	Arg	Asp	Gly	Asn	Asp	Gly	Trp	Gly	Ala	Phe	Glu	Ala
		20					25						30		

Ala	Met	Gly	Thr	Leu	Asp	Gly	Gly	Phe	Ala	Val	Ser	Tyr	Ser	Ser	Gly
		35				40						45			

Leu	Ala	Ala	Ala	Thr	Ser	Ile	Ala	Asp	Leu	Val	Pro	Thr	Gly	Gly	Thr
50						55					60				

Val Val Leu Pro Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala  
 65 70 75 80  
 Arg Met Glu Ala Arg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp  
 85 90 95  
 Asn Thr Glu Glu Val Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp  
 100 105 110  
 Val Glu Ser Ile Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala  
 115 120 125  
 Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala  
 130 135 140  
 Thr Phe Ala Thr Pro Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp  
 145 150 155 160  
 Ile Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu  
 165 170 175  
 Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Gln Phe Leu  
 180 185 190  
 Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala  
 195 200 205  
 Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg  
 210 215 220  
 Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro  
 225 230 235 240  
 Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His  
 245 250 255  
 Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser  
 260 265 270  
 Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser  
 275 280 285  
 Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala  
 290 295 300  
 Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro  
 305 310 315 320  
 Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu  
 325 330 335  
 Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly  
 340 345

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 <211> 861  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

&lt;221&gt; CDS

&lt;222&gt; (101)..(838)

&lt;223&gt; RXS03159

&lt;400&gt; 81

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tttagggcca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca 115
                                   Leu Ser Phe Asp Pro
                                   1       5

aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163
Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
              10              15              20

gac gac tac tac ggt tcg att aac acc cca atc tat gcc tcc acc acc 211
Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
              25              30              35

ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
              40              45              50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
              55              60              65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
              70              75              80              85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
              90              95              100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
              105              110              115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
              120              125              130

gaa gag gtc aag gca gcg atc aag gac aac acc aag ctg atc tgg gtg 547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Leu Ile Trp Val
              135              140              145

gaa acc cca acc aac cca gca ctt ggc atc acc gac atc gaa gca gta 595
Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr Asp Ile Glu Ala Val
              150              155              160              165

gca aag ctc acc gaa ggc acc aac gcc aag ttg gtt gtt gac aac acc 643
Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu Val Val Asp Asn Thr
              170              175              180

ttg gca tcc cca tac ctg cag cag cca cta aaa ctc ggc gca cac gca 691
Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys Leu Gly Ala His Ala
              185              190              195

agt cct tgc act cca cca cca agt aca tcg aag gac act ccg acg ttg 739
Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys Asp Thr Pro Thr Leu

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200	205	210	
ttg gcg gcc ttg tgg gta cca acg acc agg aaa tgg acg aag aac tgc			787
Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys Trp Thr Lys Asn Cys			
215	220	225	
tgt tca tgc agg gcg gca tcg gac cga tcc cat cag ttt tcg atg cat			835
Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His Gln Phe Ser Met His			
230	235	240	245
acc tgaccgccccg tggcctcaag acc			861
Thr			
<210> 82			
<211> 246			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 82			
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Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile			
20	25	30	
Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys			
35	40	45	
Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu			
50	55	60	
Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser			
65	70	75	80
Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro			
85	90	95	
Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg			
100	105	110	
Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val			
115	120	125	
Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr			
130	135	140	
Lys Leu Ile Trp Val Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr			
145	150	155	160
Asp Ile Glu Ala Val Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu			
165	170	175	
Val Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys			
180	185	190	
Leu Gly Ala His Ala Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys			
195	200	205	
Asp Thr Pro Thr Leu Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys			

210 215 220

Trp Thr Lys Asn Cys Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His  
 225 230 235 240

Gln Phe Ser Met His Thr  
 245

<210> 83  
 <211> 703  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(703)  
 <223> FRXA02768

<220>  
 <223> All occurrences of n = any nucleotide

<220>  
 <223> All occurrences of Xaa = any amino acid

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tttagggcca tagaattctg attacaggag ttgatotacc ttg tct ttt gac cca 115  
 Leu Ser Phe Asp Pro  
 1 5

aac acc cag ggt ttc tcc act gca tgc att cac gct ggg tat gag cca 163  
 Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro  
 10 15 20

gac gac tac tac ggt tgc att aac acc cca atc tat gcc tcc acc acc 211  
 Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr  
 25 30 35

ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259  
 Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr  
 40 45 50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307  
 Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala  
 55 60 65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355  
 Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala  
 70 75 80 85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403  
 Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val  
 90 95 100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451  
 Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val  
 105 110 115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499

Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val  
 120 125 130  
 gaa gag gtc aag gca gcg atc aag gac aac acc aag gct gat ctt ggt 547  
 Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Ala Asp Leu Gly  
 135 140 145  
 gga aac ccc aac caa ccc aac act ttg gca tta ccc gac atc gaa gca 595  
 Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu Pro Asp Ile Glu Ala  
 150 155 160 165  
 gtn tgc aaa act tca ccc gaa agg cac caa ccc caa gct tgt tgt ttg 643  
 Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro Gln Ala Cys Cys Leu  
 170 175 180  
 aca aca cct tcg cat tcc cca tac ctg cag can cca ctt aaa ant tnn 691  
 Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa Pro Leu Lys Xaa Xaa  
 185 190 195  
 gng cac acg cag 703  
 Xaa His Thr Gln  
 200

&lt;210&gt; 84

&lt;211&gt; 201

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;223&gt; All occurrences of Xaa = any amino acid

&lt;400&gt; 84

Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His  
 1 5 10 15  
 Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile  
 20 25 30  
 Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys  
 35 40 45  
 Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu  
 50 55 60  
 Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser  
 65 70 75 80  
 Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro  
 85 90 95  
 Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg  
 100 105 110  
 Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val  
 115 120 125  
 Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr  
 130 135 140  
 Lys Ala Asp Leu Gly Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu

145	150	155	160
Pro Asp Ile Glu Ala Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro			
	165	170	175
Gln Ala Cys Cys Leu Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa			
	180	185	190
Pro Leu Lys Xaa Xaa Xaa His Thr Gln			
	195	200	

<210> 85  
 <211> 1113  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1090)  
 <223> RXA00216

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 ttggatcagg caccatctgc cacacggagt cttaagaaaa ttg ggc gct tat ggt 115  
 Leu Gly Ala Tyr Gly  
 1 5

tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att 163  
 Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile  
 10 15 20

cag ggt gaa acg ggc gat ctt ctg cat att cct cag ctt ccg gcg cga 211  
 Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg  
 25 30 35

ggt ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg 259  
 Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met  
 40 45 50

atc aac gtt gat cgc ggg gcc cga tct tgg gtg atg agc aca cgc ccc 307  
 Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro  
 55 60 65

agc aga ttg acg cac ctg acc ggc gat ttc ctt gac atg gat ttg gat 355  
 Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp  
 70 75 80 85

gcg tgc gag gaa acc tgg gga acg ggc gtc gac aag cta aaa atc caa 403  
 Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln  
 90 95 100

gtt gct ggt ccc tgg act tta ggt gcg cgc att gag ttg gcc aat ggc 451  
 Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly  
 105 110 115

cat cgc gtt ttg tct gat cgc ggt gcg atg cgt gat ctg acg cag gcg 499  
 His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala  
 120 125 130

ctg atc gcc ggc atc gat gcg cat gca cgc aag gtt gct ggg cga ttt 547  
 Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe  
 135 140 145

cgc gcc gaa gtg cag gtg caa att gat gag ccg gag ctg aaa tcg ctt 595  
 Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu  
 150 155 160 165

atc gac ggc tcc ctc cct ggc act tcc acc ttt gac att att cct gcg 643  
 Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala  
 170 175 180

gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tcg 691  
 Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser  
 185 190 195

att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg 739  
 Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp  
 200 205 210

gat gtg gct cgg ggt gcg ggc gcc gat act gtg cag att tcc atg gat 787  
 Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp  
 215 220 225

caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc 835  
 Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr  
 230 235 240 245

agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta 883  
 Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val  
 250 255 260

gat gaa ctg ctc gag cga ccg cgg caa aag gcc gtt gag gta gca cgc 931  
 Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg  
 265 270 275

ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt 979  
 Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val  
 280 285 290

gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc 1027  
 Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala  
 295 300 305

gcg cag gct tat cgc atg gcc ccg gtg atg tcg gag atg ttg tcg aag 1075  
 Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys  
 310 315 320 325

gat tca tgc gac ctt taaggcttta ccggcgctgg gtg 1113  
 Asp Ser Cys Asp Leu  
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&lt;210&gt; 86

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 86

Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu  
 1 5 10 15

Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro  
 20 25 30  
 Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val  
 35 40 45  
 Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val  
 50 55 60  
 Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu  
 65 70 75 80  
 Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp  
 85 90 95  
 Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile  
 100 105 110  
 Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg  
 115 120 125  
 Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys  
 130 135 140  
 Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro  
 145 150 155 160  
 Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe  
 165 170 175  
 Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln  
 180 185 190  
 Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly  
 195 200 205  
 Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val  
 210 215 220  
 Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe  
 225 230 235 240  
 Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr  
 245 250 255  
 Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala  
 260 265 270  
 Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr  
 275 280 285  
 Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly  
 290 295 300  
 Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser  
 305 310 315 320  
 Glu Met Leu Ser Lys Asp Ser Cys Asp Leu  
 325 330

<210> 87  
 <211> 551  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(528)  
 <223> RXA02197

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 ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag gac 96  
 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp  
 20 25 30  
 ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct 144  
 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro  
 35 40 45  
 att cct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag 192  
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu  
 50 55 60  
 tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc 240  
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80  
 gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac qgt 288  
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95  
 gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336  
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
 100 105 110  
 ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384  
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125  
 gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt 432  
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg  
 130 135 140  
 atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc 480  
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser  
 145 150 155 160  
 aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc 528  
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val  
 165 170 175  
 taacaccttt gagagggaact act 551

<210> 88  
 <211> 176

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 88

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 1 5 10 15  
 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp  
 20 25 30  
 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro  
 35 40 45  
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu  
 50 55 60  
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80  
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95  
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
 100 105 110  
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125  
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg  
 130 135 140  
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser  
 145 150 155 160  
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val  
 165 170 175

&lt;210&gt; 89

&lt;211&gt; 2599

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2599)

&lt;223&gt; RXN02198

&lt;400&gt; 89

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 agttcgggaa ttgtctaata cgtactaagc tgtctacaca atg tct act tca gtt 115  
 Met Ser Thr Ser Val  
 1 5  
 act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163  
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala  
 10 15 20  
 ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211  
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu



25										30										35										
caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg	259																													
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly																														
40	45	50																												
tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att	307																													
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile																														
55	60	65																												
cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act	355																													
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr																														
70	75	80	85																											
ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt	403																													
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg																														
90	95	100																												
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct	451																													
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala																														
105	110	115																												
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt	499																													
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly																														
120	125	130																												
tcc ctg gga cct gga acg aag ctt cca tcc ctg ggc cat gca ccg tat	547																													
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr																														
135	140	145																												
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac	595																													
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp																														
150	155	160	165																											
ggt ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag	643																													
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln																														
170	175	180																												
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat	691																													
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp																														
185	190	195																												
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc	739																													
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr																														
200	205	210																												
atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca	787																													
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro																														
215	220	225																												
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag	835																													
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu																														
230	235	240	245																											
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg	883																													
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val																														
250	255	260																												
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca	931																													
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala																														
265	270	275																												

gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc	979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe	
280 285 290	
gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca	1027
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
295 300 305	
cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag	1075
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	
310 315 320 325	
cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag	1123
Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln	
330 335 340	
gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc	1171
Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr	
345 350 355	
tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc	1219
Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg	
360 365 370	
acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc	1267
Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly	
375 380 385	
gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt	1315
Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly	
390 395 400 405	
gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc	1363
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr	
410 415 420	
gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg	1411
Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu	
425 430 435	
cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt	1459
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu	
440 445 450	
gag cac ttg cgt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac	1507
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp	
455 460 465	
ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag	1555
Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys	
470 475 480 485	
cag cac cgt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag	1603
Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln	
490 495 500	
gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac	1651
Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp	
505 510 515	

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp 520 525 530	1699
tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp 535 540 545	1747
ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro 550 555 560 565	1795
gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn 570 575 580	1843
cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile 585 590 595	1891
gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro 600 605 610	1939
atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val 615 620 625	1987
tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln 630 635 640 645	2035
ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu 650 655 660	2083
cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile 665 670 675	2131
gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys 680 685 690	2179
gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met 695 700 705	2227
aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe 710 715 720 725	2275
gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu 730 735 740	2323
ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu 745 750 755	2371
ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat	2419

Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
 760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac 2467  
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
 775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca 2515  
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
 790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg 2563  
 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val  
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aag tcc acc gtg gtg atg aag caa acc atc agc gac 2599  
 Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser Asp  
 825 830

<210> 90  
 <211> 833  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 90  
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 35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp  
 50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu  
 65 70 75 80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr  
 85 90 95

Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val  
 100 105 110

Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg  
 115 120 125

Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu  
 130 135 140

Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala  
 145 150 155 160

Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala  
 165 170 175

Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala  
 180 185 190

Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val  
 195 200 205  
 Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu  
 210 215 220  
 Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala  
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 Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His  
 245 250 255  
 Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu  
 260 265 270  
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln  
 275 280 285  
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly  
 290 295 300  
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val  
 305 310 315 320  
 Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala  
 325 330 335  
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val  
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 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser  
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 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu  
 370 375 380  
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln  
 385 390 395 400  
 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val  
 405 410 415  
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala  
 420 425 430  
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val  
 435 440 445  
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser  
 450 455 460  
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile  
 465 470 475 480  
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile  
 485 490 495  
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala  
 500 505 510

Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys  
 515 520 525  
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu  
 530 535 540  
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu  
 545 550 555 560  
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile  
 565 570 575  
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe  
 580 585 590  
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser  
 595 600 605  
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val  
 610 615 620  
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu  
 625 630 635 640  
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys  
 645 650 655  
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu  
 660 665 670  
 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu  
 675 680 685  
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp  
 690 695 700  
 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln  
 705 710 715 720  
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala  
 725 730 735  
 Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly  
 740 745 750  
 Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys  
 755 760 765  
 Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser  
 770 775 780  
 Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser  
 785 790 795 800  
 Ala Met Leu Glu Ala Ala Glu Glu His Lys Ala Asp Val Ile Gly Met  
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 Ser Gly Leu Leu Val Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser  
 820 825 830

Asp

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<212> DNA
<213> Corynebacterium glutamicum
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Met Ser Thr Ser Val																5
1																
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Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala																20
10 15																
ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc																211
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu																35
25 30																
caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg																259
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly																50
40 45																
tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att																307
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile																65
55 60																
cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act																355
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr																85
70 75																
ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt																403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg																100
90 95																
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct																451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala																115
105 110																
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Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly																130
120 125																
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat																547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr																145
135 140																
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac																595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp																165
150 155 160																
ggg ggt ggc gat gcc ttt ttg att gag act gct cag qac ttg ctt cag																643

Gly	Gly	Gly	Asp	Ala	Phe	Leu	Ile	Glu	Thr	Ala	Gln	Asp	Leu	Leu	Gln		
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gtc	aag	gct	gcg	gtt	cac	ggc	gtt	caa	gat	gcc	atg	gct	gaa	ctt	gat	691	
Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala	Met	Ala	Glu	Leu	Asp		
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aca	ttc	ttg	ccc	att	att	tgc	cac	gtc	acc	gta	gag	acc	acc	ggc	acc	739	
Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val	Glu	Thr	Thr	Gly	Thr		
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atg	ctc	atg	ggg	tct	gag	atc	ggg	gcc	gcg	ttg	aca	gcg	ctg	cag	cca	787	
Met	Leu	Met	Gly	Ser	Glu	Ile	Gly	Ala	Ala	Leu	Thr	Ala	Leu	Gln	Pro		
	215					220					225						
ctg	ggg	atc	gac	atg	att	ggg	ctg	aac	tgc	gcc	acc	ggc	cca	gat	gag	835	
Leu	Gly	Ile	Asp	Met	Ile	Gly	Leu	Asn	Cys	Ala	Thr	Gly	Pro	Asp	Glu		
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Met	Ser	Glu	His	Leu	Arg	Tyr	Leu	Ser	Lys	His	Ala	Asp	Ile	Pro	Val		
			250						255					260			
tcg	gtg	atg	cct	aac	gca	ggg	ctt	cct	gtc	ctg	ggg	aaa	aac	ggg	gca	931	
Ser	Val	Met	Pro	Asn	Ala	Gly	Leu	Pro	Val	Leu	Gly	Lys	Asn	Gly	Ala		
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Glu	Tyr	Pro	Leu	Glu	Ala	Glu	Asp	Leu	Ala	Gln	Ala	Leu	Ala	Gly	Phe		
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gtc	tcc	gaa	tat	ggc	ctg	tcc	atg	gtg	ggg	ggg	tgt	tgt	ggc	acc	aca	1027	
Val	Ser	Glu	Tyr	Gly	Leu	Ser	Met	Val	Gly	Gly	Cys	Cys	Gly	Thr	Thr		
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cct	gag	cac	atc	cgt	gcg	gtc	cgc	gat	gcg	gtg	gtt	ggg	gtt	cca	gag	1075	
Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val	Val	Gly	Val	Pro	Glu		
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cag	gaa	acc	tcc	aca	ctg	acc	aag	atc	cct	gca	ggc	cct	gtt	gag	cag	1123	
Gln	Glu	Thr	Ser	Thr	Leu	Thr	Lys	Ile	Pro	Ala	Gly	Pro	Val	Glu	Gln		
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gcc	tcc	cgc	gag	gtg	gag	aaa	gag	gac	tcc	gtc	gcg	tcg	ctg	tac	acc	1171	
Ala	Ser	Arg	Glu	Val	Glu	Lys	Glu	Asp	Ser	Val	Ala	Ser	Leu	Tyr	Thr		
			345					350					355				
tcg	gtg	cca	ttg	tcc	cag	gaa	acc	ggc	att	tcc	atg	atc	ggg	gag	cgc	1219	
Ser	Val	Pro	Leu	Ser	Gln	Glu	Thr	Gly	Ile	Ser	Met	Ile	Gly	Glu	Arg		
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acc	aac	tcc	aac	ggg	tcc	aag	gca	ttc	cgt	gag	gca	atg	ctg	tct	ggc	1267	
Thr	Asn	Ser	Asn	Gly	Ser	Lys	Ala	Phe	Arg	Glu	Ala	Met	Leu	Ser	Gly		
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gat	tgg	gaa	aag	tgt	gtg	gat	att	gcc	aag	cag	caa	acc	cgc	gat	ggg	1315	
Asp	Trp	Glu	Lys	Cys	Val	Asp	Ile	Ala	Lys	Gln	Gln	Thr	Arg	Asp	Gly		
390					395					400					405		
gca	cac	atg	ctg	gat	ctt	tgt	gtg	gat	tac	gtg	gga	cga	gac	ggc	acc	1363	
Ala	His	Met	Leu	Asp	Leu	Cys	Val	Asp	Tyr	Val	Gly	Arg	Asp	Gly	Thr		



410	415	420	
gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu 425 430 435			1411
cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu 440 445 450			1459
gag cac ttg ggt gga cga aac atc gtt aac tcc gtc aac ttt gaa gac Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp 455 460 465			1507
ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys 470 475 480 485			1555
cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln 490 495 500			1603
gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp 505 510 515			1651
gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp 520 525 530			1699
tgc ctg acc ttc ccg atc tcc acc ggc cag gaa gaa acc agg cga gat Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp 535 540 545			1747
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gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn 570 575 580			1843
cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile 585 590 595			1891
gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro 600 605 610			1939
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tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln 630 635 640 645			2035
ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu 650 655 660			2083

cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc 2131  
 Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile  
 665 670 675  
 gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag 2179  
 Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys  
 680 685 690  
 gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg 2227  
 Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met  
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 aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc 2275  
 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe  
 710 715 720 725  
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 Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu  
 730 735 740  
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 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu  
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 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
 760 765 770  
 atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac 2467  
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
 775 780 785  
 gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca 2515  
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
 790 795 800 805  
 gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg 2563  
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 Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe  
 35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp  
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 Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu  
 65 70 75 80  
 Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr  
 85 90 95  
 Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val  
 100 105 110  
 Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg  
 115 120 125  
 Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu  
 130 135 140  
 Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala  
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 165 170 175  
 Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala  
 180 185 190  
 Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val  
 195 200 205  
 Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu  
 210 215 220  
 Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala  
 225 230 235 240  
 Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His  
 245 250 255  
 Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu  
 260 265 270  
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln  
 275 280 285  
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly  
 290 295 300  
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val  
 305 310 315 320  
 Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala  
 325 330 335  
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val  
 340 345 350  
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser  
 355 360 365  
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu

370	375	380
Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln 385 390 395 400		
Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val 405 410 415		
Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala 420 425 430		
Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val 435 440 445		
Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser 450 455 460		
Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile 465 470 475 480		
Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile 485 490 495		
Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala 500 505 510		
Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys 515 520 525		
Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu 530 535 540		
Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu 545 550 555 560		
Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile 565 570 575		
Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe 580 585 590		
Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser 595 600 605		
Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val 610 615 620		
Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu 625 630 635 640		
Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys 645 650 655		
Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu 660 665 670		
Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu 675 680 685		
Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp 690 695 700		

Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln  
 705 710 715 720  
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala  
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 Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly  
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 Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys  
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 Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser  
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 Met Thr Gln Ser Ala  
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 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
 10 15 20  
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35  
 ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
 40 45 50  
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
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 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala

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Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala				
	90	95	100	
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Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala				
	105	110	115	
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Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg				
	120	125	130	
gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac				547
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr				
	135	140	145	
gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag				595
Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys				
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cag taatttgttt tgacgacgca gta				621
Gln				

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&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 94

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
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Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
20 25 30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
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145                      150                      155                      160

Glu Ala Pro Ile Lys Gln  
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Met Thr Gln Ser Ala  
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cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
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gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
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ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
120 125 130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
135 140 145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys

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 Gln

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 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
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 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
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 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
                     65                    70                    75                    80  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
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 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
                     100                    105                    110  
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
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 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
                     130                    135                    140  
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 Glu Ala Pro Ile Lys Gln  
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																1				5	
gac	ttc	aag	gtt	gcc	gat	ctt	tca	cta	gca	gag	gca	gga	cgt	cac	cag	163					
Asp	Phe	Lys	Val	Ala	Asp	Leu	Ser	Leu	Ala	Glu	Ala	Gly	Arg	His	Gln						
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Ile	Arg	Leu	Ala	Glu	Tyr	Glu	Met	Pro	Gly	Leu	Met	Gln	Leu	Arg	Lys						
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Glu	Phe	Ala	Asp	Glu	Gln	Pro	Leu	Lys	Gly	Ala	Arg	Ile	Ala	Gly	Ser						
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Ile	His	Met	Thr	Val	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu	Thr	Ala						
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Leu	Gly	Ala	Glu	Val	Arg	Trp	Ala	Ser	Cys	Asn	Ile	Phe	Ser	Thr	Gln						
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Asp	Glu	Ala	Ala	Ala	Ala	Ile	Val	Val	Gly	Ser	Gly	Thr	Val	Glu	Glu						
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Pro	Ala	Gly	Val	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Ser	Leu	Glu	Glu						
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Tyr	Trp	Trp	Cys	Ile	Asn	Gln	Ile	Phe	Ser	Trp	Gly	Asp	Glu	Leu	Pro						
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aac	atg	atc	ctc	gac	gac	ggc	ggc	gac	gcc	acc	atg	gct	gtt	att	cgc	547					
Asn	Met	Ile	Leu	Asp	Asp	Gly	Gly	Asp	Ala	Thr	Met	Ala	Val	Ile	Arg						
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ggc	cgc	gaa	tac	gag	cag	gct	ggc	ctg	gtt	cca	cca	gca	gag	gcc	aac	595					
Gly	Arg	Glu	Tyr	Glu	Gln	Ala	Gly	Leu	Val	Pro	Pro	Ala	Glu	Ala	Asn						
				150					155					160							
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Asp	Ser	Asp	Glu	Tyr	Ile	Ala	Phe	Leu	Gly	Met	Leu	Arg	Glu	Val	Leu						
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gct	gca	gag	cct	ggc	aag	tgg	ggc	aag	atc	gct	gag	gcc	gtt	aag	ggc	691					
Ala	Ala	Glu	Pro	Gly	Lys	Trp	Gly	Lys	Ile	Ala	Glu	Ala	Val	Lys	Gly						
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Val	Thr	Glu	Glu	Thr	Thr	Thr	Gly	Val	His	Arg	Leu	Tyr	His	Phe	Ala						
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gaa	gaa	ggc	gtg	ctg	cct	ttc	cca	gcg	atg	aac	gtc	aac	gac	gct	gtc	787					
Glu	Glu	Gly	Val	Leu	Pro	Phe	Pro	Ala	Met	Asn	Val	Asn	Asp	Ala	Val						
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acc	aag	tcc	aag	ttt	gat	aac	aag	tac	ggc	acc	cgc	cac	tcc	ctg	atc	835					
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ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe	265	270	275	931
gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn	280	285	290	979
gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu	295	300	305	1027
gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp	310	315	320	1075
atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu	330	335	340	1123
ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu	345	350	355	1171
cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu	360	365	370	1219
ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg	375	380	385	1267
ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser	390	395	400	1315
aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn	410	415	420	1363
gaa gga cag tac gag aac gag gtc tac cgt ctg cct aag gtt ctc gac Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp	425	430	435	1411
gaa aag gtg gca cgc atc cac gtt gag gct ctc ggc ggt cag ctc acc Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr	440	445	450	1459
gaa ctg acc aag gag cag gct gag tac atc ggc gtt gac gtt gca ggc Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly	455	460	465	1507
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 Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile  
 50 55 60  
 Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn  
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 Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser  
 85 90 95  
 Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly  
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 Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp  
 115 120 125  
 Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr  
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 Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro  
 145 150 155 160  
 Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met  
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 Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala  
 180 185 190  
 Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg  
 195 200 205  
 Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn  
 210 215 220  
 Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr  
 225 230 235 240  
 Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met  
 245 250 255  
 Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly  
 260 265 270  
 Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu  
 275 280 285

Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val  
 290 295 300

Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala  
 305 310 315 320

Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys  
 325 330 335

Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp  
 340 345 350

Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys  
 355 360 365

Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val  
 370 375 380

Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro  
 385 390 395 400

Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile  
 405 410 415

Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu  
 420 425 430

Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu  
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 <213> Corynebacterium glutamicum

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 <223> FRXA00132

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gct gag tac atc ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac 96  
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His  
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tac cgc tac taatgattgt cagcattgag gga 128  
 Tyr Arg Tyr  
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Tyr Arg Tyr
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gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val 215 220 225	787
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gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val 250 255 260	883
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 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg  
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 115 120 125  
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 130 135 140  
 Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro  
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 Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met  
 165 170 175  
 Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala

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Val	Asn	Asp	Ala	Val	Thr	Lys	Ser	Lys	Phe	Asp	Asn	Lys	Tyr	Gly	Thr
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Arg	His	Ser	Leu	Ile	Asp	Gly	Ile	Asn	Arg	Ala	Thr	Asp	Met	Leu	Met
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Cys	Ala	Glu	Ala	Phe	Asp	Gly	Gln	Gly	Ala	Arg	Val	Lys	Val	Thr	Glu
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Pro	Gln	Val	Asp	Glu	Phe	Thr	Phe	Ser	Thr	Gly	Arg	Ser	Ile	Ile	Val
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&lt;210&gt; 103

&lt;211&gt; 2358

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2335)

&lt;223&gt; RXN02085

&lt;400&gt; 103

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	1 5	
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Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala		
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Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg		
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135 140 145		
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Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro		
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Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys		
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Val	Asp	Leu	Val	Thr	His	Gly	Val	Thr	Glu	Leu	Ala	Ala	Trp	Lys	Gly		
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Glu	Glu	Leu	Leu	Val	Ala	Gly	Ile	Val	Asp	Gly	Arg	Asn	Ile	Trp	Arg		
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Gly	Pro	Ile	Ala	Val	Ser	Thr	Ser	Cys	Ser	Leu	Leu	His	Val	Pro	Tyr		
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Thr	Leu	Glu	Ala	Glu	Asn	Ile	Glu	Pro	Glu	Val	Arg	Asp	Trp	Leu	Ala		
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Phe	Gly	Ser	Glu	Lys	Ile	Thr	Glu	Val	Lys	Leu	Leu	Ala	Asp	Ala	Leu		
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gct	tct	cga	cgc	acc	tcc	cca	cgc	acc	gca	cca	atc	acg	cag	gaa	ctc		1267
Ala	Ser	Arg	Arg	Thr	Ser	Pro	Arg	Thr	Ala	Pro	Ile	Thr	Gln	Glu	Leu		
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cct	ggc	cgt	agc	cgt	gga	tcc	ttc	gac	act	cgt	gtt	acg	ctg	cag	gag		1315
Pro	Gly	Arg	Ser	Arg	Gly	Ser	Phe	Asp	Thr	Arg	Val	Thr	Leu	Gln	Glu		
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Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe		
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Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala	Arg	Leu	Arg	Lys	Glu		
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Ser	Ile	Thr	Leu	Glu	Gln	Tyr	Glu	Glu	Ala	Met	Arg	Glu	Glu	Ile	Asp		
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ctg	gtc	atc	gcc	aag	cag	gaa	gaa	ctt	ggc	ctt	gat	gtg	ttg	gtt	cac		1507
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ggc	gag	cca	gag	cgc	aac	gac	atg	gtt	cag	tac	ttc	tct	gaa	ctt	ctc		1555
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	505	510	515	
cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag	Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys	1699		
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ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca	Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala	1795		
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ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag	Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys	1843		
	570	575	580	
atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga	Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg	1891		
	585	590	595	
gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc	Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg	1939		
	600	605	610	
ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg	Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met	1987		
	615	620	625	
tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat	Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp	2035		
	630	635	640	645
gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc	Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu	2083		
	650	655	660	
gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg	Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val	2131		
	665	670	675	
tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt	Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly	2179		
	680	685	690	
ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc	Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val	2227		
	695	700	705	
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	710	715	720	725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc 2323  
 Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile  
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<400> 104

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                     20                    25                    30  
 Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
                     35                    40                    45  
 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
                     50                    55                    60  
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
   65                    70                    75                    80  
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
                     85                    90                    95  
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
                     100                    105                    110  
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
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 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
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 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
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 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
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 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
                     180                    185                    190  
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
                     195                    200                    205  
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
                     210                    215                    220  
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
   225                    230                    235                    240

148

565										570					575				
Glu	Ala	Gly	Ala	Lys	Ile	Ile	Gln	Val	Asp	Glu	Pro	Ala	Ile	Arg	Glu				
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Leu	Leu	Pro	Leu	Arg	Asp	Val	Asp	Lys	Pro	Ala	Tyr	Leu	Gln	Trp	Ser				
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Val	Asp	Ser	Phe	Arg	Leu	Ala	Thr	Ala	Gly	Ala	Pro	Asp	Asp	Val	Gln				
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Ile	His	Thr	His	Met	Cys	Tyr	Ser	Glu	Phe	Asn	Glu	Val	Ile	Ser	Ser				
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Val	Ile	Ala	Leu	Asp	Ala	Asp	Val	Thr	Thr	Ile	Glu	Ala	Ala	Arg	Ser				
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Asp	Met	Gln	Val	Leu	Ala	Ala	Leu	Lys	Ser	Ser	Gly	Phe	Glu	Leu	Gly				
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Val	Gly	Pro	Gly	Val	Trp	Asp	Ile	His	Ser	Pro	Arg	Val	Pro	Ser	Ala				
	675						680					685							
Gln	Lys	Val	Asp	Gly	Leu	Leu	Glu	Ala	Ala	Leu	Gln	Ser	Val	Asp	Pro				
	690					695					700								
Arg	Gln	Leu	Trp	Val	Asn	Pro	Asp	Cys	Gly	Leu	Lys	Thr	Arg	Gly	Trp				
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Pro	Glu	Val	Glu	Ala	Ser	Leu	Lys	Val	Leu	Val	Glu	Ser	Ala	Lys	Gln				
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 Met Thr Ser Asn Phe  
 1 5  
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 Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu  
 10 15 20  
 aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211  
 Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu  
 25 30 35

ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg	259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu	
40 45 50	
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Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	
55 60 65	
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat	355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp	
70 75 80 85	
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
90 95 100	
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
105 110 115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
120 125 130	
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
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Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
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Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
170 175 180	
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Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
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Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
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Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
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Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
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Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
250 255 260	
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
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Thr	Asp	Leu	Cys	Ala	Ala	Leu	Ala	Ser	Leu	Lys	Arg	Leu	Ala	Ala	Arg		
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Thr	Leu	Glu	Ala	Glu	Asn	Ile	Glu	Pro	Glu	Val	Arg	Asp	Trp	Leu	Ala		
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Phe	Gly	Ser	Glu	Lys	Ile	Thr	Glu	Val	Lys	Leu	Leu	Ala	Asp	Ala	Leu		
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gcc	ggc	aac	atc	gac	gcg	gct	gcg	ttc	gat	gcg	gcg	tcc	gca	gca	att	1219	
Ala	Gly	Asn	Ile	Asp	Ala	Ala	Ala	Phe	Asp	Ala	Ala	Ser	Ala	Ala	Ile		
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gct	tct	cga	cgc	acc	tcc	cca	cgc	acc	gca	cca	atc	acg	cag	gaa	ctc	1267	
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Pro	Gly	Arg	Ser	Arg	Gly	Ser	Phe	Asp	Thr	Arg	Val	Thr	Leu	Gln	Glu		
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aag	tca	ctg	gag	ctt	cca	gct	ctg	cca	acc	acc	acc	att	ggt	tct	ttc	1363	
Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe		
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cca	cag	acc	cca	tcc	att	cgt	tct	gct	cgc	gct	cgt	ctg	cgc	aag	gaa	1411	
Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala	Arg	Leu	Arg	Lys	Glu		
			425					430					435				
tcc	atc	act	ttg	gag	cag	tac	gaa	gag	gca	atg	cgc	gaa	gaa	atc	gat	1459	
Ser	Ile	Thr	Leu	Glu	Gln	Tyr	Glu	Glu	Ala	Met	Arg	Glu	Glu	Ile	Asp		
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Leu	Val	Ile	Ala	Lys	Gln	Glu	Glu	Leu	Gly	Leu	Asp	Val	Leu	Val	His		
		455					460				465						
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Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met	Val	Gln	Tyr	Phe	Ser	Glu	Leu	Leu		
		470				475				480					485		
gac	ggt	ttc	ctc	tca	acc	gcc	aac	ggc	tgg	gtc	caa	agc	tac	ggc	tcc	1603	
Asp	Gly	Phe	Leu	Ser	Thr	Ala	Asn	Gly	Trp	Val	Gln	Ser	Tyr	Gly	Ser		
				490					495					500			
cgc	tgt	gtt	cgt	cct	cca	gtg	ttg	ttc	gga	aac	gtt	tcc	cgc	cca	gcg	1651	
Arg	Cys	Val	Arg	Pro	Pro	Val	Leu	Phe	Gly	Asn	Val	Ser	Arg	Pro	Ala		
			505					510					515				
cca	atg	act	gtc	aag	tgg	ttc	cag	tac	gca	cag	agc	ctg	acc	cag	aag	1699	
Pro	Met	Thr	Val	Lys	Trp	Phe	Gln	Tyr	Ala	Gln	Ser	Leu	Thr	Gln	Lys		



520	525	530	
cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser 535 540 545			1747
ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca Phe Val Arg Asp Asp Glu Pro Leu Ala Thr Thr Ala Asp Gln Val Ala 550 555 560 565			1795
ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys 570 575 580			1843
atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr 585 590 595			1891
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&lt;210&gt; 106

&lt;211&gt; 600

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 106

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Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg 50 55 60
Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu 65 70 75 80
Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro 85 90 95
Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu 100 105 110
Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu 115 120 125
Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala 130 135 140
Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg 145 150 155 160
Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr 165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
 180 185 190  
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
 195 200 205  
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
 210 215 220  
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
 225 230 235 240  
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
 245 250 255  
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
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 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
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 305 310 315 320  
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 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
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 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro  
 370 375 380  
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 385 390 395 400  
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr  
 405 410 415  
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala  
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 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met  
 435 440 445  
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu  
 450 455 460  
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr  
 465 470 475 480  
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val  
 485 490 495

Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn  
 500 505 510

Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln  
 515 520 525

Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr  
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Ala Asp Cln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile  
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 Met Ser Leu Arg Phe  
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 Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln  
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 Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp  
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 Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile  
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 Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala  
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 Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu  
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Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val				
	105	110	115	
gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt				499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg				
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Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala				
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 Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu  
 35 40 45  
 Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr  
 50 55 60  
 Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys  
 65 70 75 80  
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His  
 85 90 95  
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala  
 100 105 110  
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys  
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 <212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1303)

&lt;223&gt; RXN02648

&lt;400&gt; 109

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                                         1           5

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Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
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Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
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Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
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gac ctg cgt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly Gly His Val Thr
                        55                60                65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
                        70                75                80                85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
                        90                95                100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
                        105                110                115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
                        120                125                130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
                        135                140                145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
                        150                155                160                165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
                        170                175                180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
                        185                190                195

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act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739  
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu  
 200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca ccg 787  
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro  
 215 220 225

gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag 835  
 Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys  
 230 235 240 245

gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca 883  
 Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala  
 250 255 260

gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc 931  
 Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly  
 265 270 275

tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att 979  
 Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile  
 280 285 290

ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca 1027  
 Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala  
 295 300 305

tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt 1075  
 Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu  
 310 315 320 325

cct gaa ggc lct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac 1123  
 Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn  
 330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc 1171  
 Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala  
 345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg 1219  
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu  
 360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta 1267  
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu  
 375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac 1313  
 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 390 395 400

aacgagggtt gct 1326

&lt;210&gt; 110

&lt;211&gt; 401

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 110

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Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1           5           10           15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
          20           25           30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35           40           45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50           55           60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65           70           75           80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
          85           90           95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
          100          105          110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
          115          120          125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
          130          135          140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
          145          150          155          160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
          165          170          175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
          180          185          190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
          195          200          205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
          210          215          220

Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
          225          230          235          240

Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
          245          250          255

Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
          260          265          270

His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
          275          280          285

Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
          290          295          300

Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
          305          310          315          320

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Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val  
 325 330 335

Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg  
 340 345 350

Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser  
 355 360 365

Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala  
 370 375 380

Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu  
 385 390 395 400

Phe

<210> 111  
 <211> 548  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(525)  
 <223> FRXA02648

<400> 111  
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 Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro  
 1 5 10 15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96  
 Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile  
 20 25 30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144  
 Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
 35 40 45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192  
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
 50 55 60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240  
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
 65 70 75 80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288  
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
 85 90 95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336  
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His  
 100 105 110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384  
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
 115 120 125



cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432  
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
 130 135 140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480  
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
 145 150 155 160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525  
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 165 170 175

taagctagac aacgagggtt gct 548

<210> 112

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro  
 1 5 10 15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile  
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His  
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 165 170 175

<210> 113

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(784)

&lt;223&gt; FRXA02658

&lt;400&gt; 113

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gagtttgata ctttcttttcg acttttagat tggattttca atg agc cag aac cgc 115
                                         Met Ser Gln Asn Arg
                                         1           5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
                        10                        15                        20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
                        25                        30                        35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
                        40                        45                        50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
                        55                        60                        65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
                        70                        75                        80                        85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
                        90                        95                        100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
                        105                        110                        115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
                        120                        125                        130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
                        135                        140                        145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
                        150                        155                        160                        165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
                        170                        175                        180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
                        185                        190                        195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739

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Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu  
 200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784  
 Tyr Lys. Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala  
 215 220 225

<210> 114

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 114

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
 210 215 220

Gln Leu Asp Ala  
 225

<210> 115



Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile  
65 70 75 80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
85 90 95

<210> 117

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

<400> 117

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cgttgatcgc tccagagaca ccg-ggggaag gggagcagca gtg agt aaa att tcg 115  
Val Ser Lys Ile Ser  
1 5

acg aaa ctg aag gcc ctg acc gcg gtg ctg tct gtg acc act ctg gtg 163  
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val  
10 15 20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211  
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg  
25 30 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259  
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro  
40 45 50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307  
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala  
55 60 65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355  
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly  
70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403  
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg  
90 95 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451  
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile  
105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctg agc ggt ggc gtg tat 499  
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr  
120 125 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa 547  
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu  
135 140 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595

Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu	
150 155 160 165	
aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt	643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe	
170 175 180	
gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat	691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	
185 190 195	
gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt	739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly	
200 205 210	
cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat	787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp	
215 220 225	
gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg	835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu	
230 235 240 245	
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg	883
Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val	
250 255 260	
tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct	931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala	
265 270 275	
gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac	979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp	
280 285 290	
ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg	1027
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu	
295 300 305	
ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg	1075
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val	
310 315 320 325	
agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg	1123
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala	
330 335 340	
att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac	1171
Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn	
345 350 355	
gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg	1219
Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala	
360 365 370	
ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt	1267
Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser	
375 380 385	
ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga	1315
Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg	

390	395	400	405	
tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg				1363
Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu	410	415	420	
cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act				1411
Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr	425	430	435	
ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc				1459
Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val	440	445	450	
gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag				1507
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu	455	460	465	
gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca				1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro	470	475	480	485
gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg				1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp	490	495	500	
cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat				1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn	505	510	515	
ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac				1699
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr	520	525	530	
gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat				1747
Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp	535	540	545	
att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg				1795
Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val	550	555	560	565
gtt gcg tac tga tggagct gttcttcccg cgc				1827
Val Ala Tyr				

&lt;210&gt; 118

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 118

Val	Ser	Lys	Ile	Ser	Thr	Lys	Leu	Lys	Ala	Leu	Thr	Ala	Val	Leu	Ser
1				5					10					15	

Val	Thr	Thr	Leu	Val	Ala	Gly	Cys	Ser	Thr	Leu	Pro	Gln	Asn	Thr	Asp
			20					25					30		

Pro	Gln	Val	Leu	Arg	Ser	Phe	Ser	Gly	Ser	Gln	Ser	Thr	Gln	Glu	Ile
		35					40					45			

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe  
 50 55 60  
 Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala  
 65 70 75 80  
 Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr  
 85 90 95  
 Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn  
 100 105 110  
 Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu  
 115 120 125  
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile  
 130 135 140  
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp  
 145 150 155 160  
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His  
 165 170 175  
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg  
 180 185 190  
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala  
 195 200 205  
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn  
 210 215 220  
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr  
 225 230 235 240  
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe  
 245 250 255  
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro  
 260 265 270  
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr  
 275 280 285  
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn  
 290 295 300  
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val  
 305 310 315 320  
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp  
 325 330 335  
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val  
 340 345 350  
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly  
 355 360 365



Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe  
 370 375 380  
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro  
 385 390 395 400  
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu  
 405 410 415  
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe  
 420 425 430  
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys  
 435 440 445  
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val  
 450 455 460  
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser  
 465 470 475 480  
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro  
 485 490 495  
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser  
 500 505 510  
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser  
 515 520 525  
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro  
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 545 550 555 560  
 Arg Ala Ala Pro Val Val Ala Tyr  
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<210> 119  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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<400> 119  
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aagactattt attctcaact tcttcgaaag aagggtattt gtg gct cag cca acc 115  
 Val Ala Gln Pro Thr  
 1 5

gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163  
 Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp  
 10 15 20

aaa ata tgt gat gct att tcc gat acc att ttg gac gcg ctg ctc gaa	211
Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu	
25 30 35	
aaa gat ccg cag tcg cgc gtc gca gtg gaa act gtg gtc acc acc gga	259
Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly	
40 45 50	
atc gtc cat gtt gtt ggc gag gtc cgt acc agc gct tac gta gag atc	307
Ile Val His Val Val Gly Glu Val Arg Thr Ser Ala Tyr Val Glu Ile	
55 60 65	
cct caa tta gtc cgc aac aag ctc atc gaa atc gga ttc aac tcc tct	355
Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile Gly Phe Asn Ser Ser	
70 75 80 85	
gag gtt gga ttc gac gga cgc acc tgt ggc gtc tca gta tcc atc ggt	403
Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val Ser Val Ser Ile Gly	
90 95 100	
gag cag tcc cag gaa atc gct gac ggc gtg gat aac tcc gac gaa gcc	451
Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Asn Ser Asp Glu Ala	
105 110 115	
cgc acc aac ggc gac gtt gaa gaa gac gac cgc gca ggt gct ggc gac	499
Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg Ala Gly Ala Gly Asp	
120 125 130	
cag ggc ctg atg ttc ggc tac gcc acc aac gaa acc gaa gag tac atg	547
Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu Thr Glu Glu Tyr Met	
135 140 145	
cct ctt cct atc gcg ttg gcg cac cga ctg tca cgt cgt ctg acc cag	595
Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser Arg Arg Leu Thr Gln	
150 155 160 165	
gtt cgt aaa gag ggc atc gtt cct cac ctg cgt cca gac gga aaa acc	643
Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr	
170 175 180	
cag gtc acc ttc gca tac gat gcg caa gac cgc cct agc cac ctg gat	691
Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp	
185 190 195	
acc gtt gtc atc tcc acc cag cac gac cca gaa gtt gac cgt gca tgg	739
Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp	
200 205 210	
ttg gaa acc caa ctg cgc gaa cac gtc att gat tgg gta atc aaa gac	787
Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp	
215 220 225	
gca ggc att gag gat ctg gca acc ggt gag atc acc gtg ttg atc aac	835
Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn	
230 235 240 245	
cct tca ggt tcc ttc att ctg ggt ggc ccc atg ggt gat gcg ggt ctg	883
Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu	
250 255 260	
acc ggc cgc aag atc atc gtg gat acc tac ggt ggc atg gct cgc cat	931

Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His  
 265 270 275  
 ggt ggt gga gca ttc tcc ggt aag gat cca agc aag gtg gac cgc tct 979  
 Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser  
 280 285 290  
 gct gca tac gcc atg cgt tgg gta gca aag aac atc gtg gca gca ggc 1027  
 Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly  
 295 300 305  
 ctt gct gat cgc gct gaa gtt cag gtt gca tac gcc att gga cgc gca 1075  
 Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala  
 310 315 320 325  
 aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc 1123  
 Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly  
 330 335 340  
 ctg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg 1171  
 Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu  
 345 350 355  
 cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac 1219  
 Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr  
 360 365 370  
 gct gac act gct gcc tac ggc cac ttt ggt cgc act gat ttg gac ctt 1267  
 Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu  
 375 380 385  
 cct tgg qag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctc aag 1315  
 Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys  
 390 395 400 405  
 ttg gcc taaaaatctg atgtagtattc ttc 1344  
 Leu Ala

&lt;210&gt; 120

&lt;211&gt; 407

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 120

Val Ala Gln Pro Thr Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr  
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Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu  
 20 25 30

Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr  
 35 40 45

Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser  
 50 55 60

Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile  
 65 70 75 80

Gly Phe Asn Ser Ser Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val  
                             85                            90                            95  
 Ser Val Ser Ile Gly Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp  
                             100                            105                            110  
 Asn Ser Asp Glu Ala Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg  
                             115                            120                            125  
 Ala Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu  
                             130                            135                            140  
 Thr Glu Glu Tyr Met Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser  
                             145                            150                            155                            160  
 Arg Arg Leu Thr Gln Val Arg Lys Glu Gly Ile Val Pro His Leu Arg  
                             165                            170                            175  
 Pro Asp Gly Lys Thr Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg  
                             180                            185                            190  
 Pro Ser His Leu Asp Thr Val Val Ile Ser Thr Gln His Asp Pro Glu  
                             195                            200                            205  
 Val Asp Arg Ala Trp Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp  
                             210                            215                            220  
 Trp Val Ile Lys Asp Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile  
                             225                            230                            235                            240  
 Thr Val Leu Ile Asn Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met  
                             245                            250                            255  
 Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly  
                             260                            265                            270  
 Gly Met Ala Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser  
                             275                            280                            285  
 Lys Val Asp Arg Ser Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn  
                             290                            295                            300  
 Ile Val Ala Ala Gly Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr  
                             305                            310                            315                            320  
 Ala Ile Gly Arg Ala Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp  
                             325                            330                            335  
 Thr Asn Lys Glu Gly Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu  
                             340                            345                            350  
 Glu Val Phe Asp Leu Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu  
                             355                            360                            365  
 Leu Arg Pro Ile Tyr Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg  
                             370                            375                            380  
 Thr Asp Leu Asp Leu Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu  
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 Arg Ala Ala Leu Lys Leu Ala

405

<210> 121  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 121  
tcgggtatcc gcgctacactt aga 23

<210> 122  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 122  
GGAAACCGGG GCATCGAAAC TTA 23

<210> 123  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 123  
ggaaacagta tgaccatg 18

<210> 124  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 124  
gtaaaacgac ggccagt 18

<210> 125  
<211> 4334  
<212> DNA  
<213> Corynebacterium glutamicum

<400> 125  
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gacaatcaat gaagctatgt ctgaatttag cgtgtcacgt cagaccgtga atagagcact 120

taagtctgcg ggcattgaac ttccacgagg acgccgtaaa gcttcccagt aaatgtgcca 180  
tctcgtaggc agaaaacggt tcccccgta ggggtctctc tcttgccctc ctttctaggt 240  
cgggctgatt gctcttgaag ctctctaggg gggctcacac cataggcaga taacggttcc 300  
ccaccggctc acctcgtaag cgcacaagga ctgctcccaa agatcttcaa agccactgcc 360  
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